

Sequences and diallelic markers thereof
Patent: WO 0100803-A 4 04-JAN-2001;

JOURNAL

GENSET (FR)

Location/Qualifiers

FEATURES

source 1..5381

/organism="Homo sapiens"

/db_xref="taxon:9606"

misc_feature

1..918

/note="5' regulatory region"

primer_bind

300..318

/note="17-42-319.mis"

misc_feature

307..331

/note="17-42-319.probe"

variation

319

/note="17-42-319 : polymorphic base C or T"

primer_bind

320..338

/note="17-42-319.mis complement"

exon

919..930

/note="exon 1"

variation

1241

/replace="T"

exon

1442..1498

/note="exon 2"

variation

1447

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exon

1613..1724

/replace="G"

exon

2243..3940

/note="exon 3"

exon

3194..3212

/note="exon 4"

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misc_feature

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/note="17-41-250.mis"

variation

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/note="17-41-250 : polymorphic base C or T"

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3214..3232

/note="17-41-250.mis complement"

misc_feature

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/note="3' regulatory region"

BASE COUNT

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ORIGIN

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99.7%: Score 120.6; DB 6; Length 5381;

Best Local Similarity 100.0%; Pred. No. 2.6e-27;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GCATTTGGGCTTGCCTCTCCAGAGGCGCCGCGAGTTCAGCTTTTCCTCATGGGG 60

Db 252 GCATTTGGGCTTGCCTCTCCAGAGGCGCCGCGAGTTCAGCTTTTCCTCATGGGG 311

Qy 61 CAATCTTACTTTCCTCCAGTTCCTGGGGCTCAGAGTCCCTGGCCAGATGCTCTTGC 120

Db 312 CAATCTTACTTTCCTCCAGTTCCTGGGGCTCAGAGTCCCTGGCCAGATGCTCTTGC 371

Qy 121 C 121

Db 372 C 372

RESULT 2

AX469879

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

ORGANISM

REFERENCE

AUTHORS Bouguetel, L., Duclert, A., Clusel, C., Dumas, M.E., Yen-Potin, P.,
Denison, B., Blahin, B., Bour, B., Ebbers, R., and Salter, Cld. L.
TITLE Methods and compositions for inhibiting neoplastic cell growth
JOURNAL Patent: WO 0205734-A 4 11-JUL-2002;

FEATURES

source 1..5381

/organism="Homo sapiens"

misc_feature

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/note="5' regulatory region"

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/note="17-42-319.mis"

misc_binding

307..331

/note="17-42-319.probe"

variation

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/note="17-42-319 : polymorphic base C or T"

primer_bind

320..338

/note="17-42-319.mis complement"

exon

919..930

/note="exon 1"

variation

1241

/replace="T"

exon

1442..1498

/note="exon 2"

variation

1447

/note="17-40-202 : G in ref genbank AC007707"

exon

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/number=3

exon

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/number=4

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/note="17-41-250.mis"

misc_binding

3201..3225

/note="17-41-250.mis"

variation

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/note="17-41-250 : polymorphic base C or T"

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/note="17-41-250.mis complement"

misc_feature

3941..5381

/note="3' regulatory region"

BASE COUNT

1104 a 1434 c 1709 g 1132 t 2 others

ORIGIN

Query Match

99.7%: Score 120.6; DB 6; Length 5381;

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Db 1 GCATTTGGGCTTGCCTCTCCAGAGGCGCCGCGAGTTCAGCTTTTCCTCATGGGG 60

Db 252 GCATTTGGGCTTGCCTCTCCAGAGGCGCCGCGAGTTCAGCTTTTCCTCATGGGG 311

Qy 61 CAATCTTACTTTCCTCCAGTTCCTGGGGCTCAGAGTCCCTGGCCAGATGCTCTTGC 120

Db 312 CAATCTTACTTTCCTCCAGTTCCTGGGGCTCAGAGTCCCTGGCCAGATGCTCTTGC 371

Qy 121 C 121

Db 372 C 372

RESULT 3

AX063464

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

ORGANISM

REFERENCE

AUTHORS Bouguetel, L., Duclert, A., Clusel, C., Dumas, M.E., Yen-Potin, P.,
Denison, B., Blahin, B., Bour, B., Ebbers, R., and Salter, Cld. L.
TITLE Methods and compositions for inhibiting neoplastic cell growth
JOURNAL Patent: WO 0205734-A 4 11-JUL-2002;

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320..338

/note="17-42-319.mis complement"

exon

919..930

/note="exon 1"

variation

1241

/replace="T"

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1442..1498

/note="exon 2"

variation

1447

/note="17-40-202 : G in ref genbank AC007707"

exon

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/number=3

exon

2243..3940

/number=4

primer_bind

3194..3212

/note="17-41-250.mis"

misc_binding

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/note="17-41-250.mis"

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primer_bind

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/note="3' regulatory region"

BASE COUNT

1104 a 1434 c 1709 g 1132 t 2 others

ORIGIN

Query Match

99.7%: Score 120.6; DB 6; Length 5381;

Best Local Similarity 100.0%; Pred. No. 2.6e-27;

Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GCATTTGGGCTTGCCTCTCCAGAGGCGCCGCGAGTTCAGCTTTTCCTCATGGGG 60

Db 252 GCATTTGGGCTTGCCTCTCCAGAGGCGCCGCGAGTTCAGCTTTTCCTCATGGGG 311

Qy 61 CAATCTTACTTTCCTCCAGTTCCTGGGGCTCAGAGTCCCTGGCCAGATGCTCTTGC 120

Db 312 CAATCTTACTTTCCTCCAGTTCCTGGGGCTCAGAGTCCCTGGCCAGATGCTCTTGC 371

Qy 121 C 121

Db 372 C 372

RESULT 3

AX063464

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

ORGANISM

REFERENCE

AUTHORS Yen, F., Denison, B., Bour, B., Bihain, B., Bougueleret, L., Duclet, A. and dumas milne Edwards, J.B.
 TITLE Apolipoprotein a-iv-related protein: polypeptide, polynucleotide sequences and biallelic markers thereof
 JOURNAL Patent: WO 0100803-A 1 04-JAN-2001;
 GENSET (FR)

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 1357. 1377
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 15229. 15253
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 Best local Similarity 100.0% ; Pred. No. 2.5e-27 ;
 Matches 121 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
 QY 1 GCATTGGGCTTGCTCTCTCAGAGGCCCTGCGAGTGAAGTTCAGCTTTTCCATCGGG 60
 Db 12280 GCATTGGGCTTGCTCTCTCAGAGGCCCTGCGAGTGAAGTTCAGCTTTTCCATCGGG 12339
 QY 61 CAATCTTACTTTCGCTCCAGTTCCTGGGGCTGAGTCCCTGGCCAGATGCTCTTGC 120
 Db 12340 CAATCTTACTTTCGCTCCAGTTCCTGGGGCTGAGTCCCTGGCCAGATGCTCTTGC 12399
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 Db 12400 c 12400

RESULT 4
 LOCUS AX469876 81001 bp DNA linear PAT 09-AUG-2002
 DEFINITION Sequence 1 from Patent WO02053734.
 ACCESSION AX469876
 VERSION AX469876.1 GI:22205149
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 AUTHORS Bougueleret, L., Duclet, A., Clusel, C., Dumas, M.E., Yen-Potin, F.,
 Denison, B., Bihain, B., Bour, B., Ebberts-Reed, D. and Salter-Cid, L.
 TITLE Methods and compositions for inhibiting neoplastic cell growth
 JOURNAL Patent: WO 02053734-A 1 11-JUL-2002;
 GENSET SA (FR)
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 1220. 1238
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variation         /note="17-41-250 : polymorphic base C or T"
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                  15969..17969
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                  42206..42230
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variation         /note="20-841-149 : polymorphic base A or G"
                  42219..42237
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                  77166..77185
primer_bind       /note="20-853.rp complement"

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BASE COUNT      20291 a 17705 c 19080 g 23919 t      6 others
ORIGIN
Query Match      99.7%; Score 120.6; DB 6; Length 81001;
Best Local Similarity 100.0%; Pred. No. 2,5e-27;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 GCATTGGGCTTGCTGCTCCAGAGGCCGCGAGTGGAGTTCAGTTCTTCATGCGG 60
          |||
Db      12280 GCATTGGGCTTGCTGCTCCAGAGGCCGCGAGTGGAGTTCAGTTCTTCATGCGG 12339
QY      61 CAATCTTACTTTCGCTCCAGATTCCTGGGCTCAGAGTCCCTGGCCAGATGCTTTGC 120
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QY      121 C 121
Db      12400 C 12400

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RESULT 5
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LOCUS           Homo sapiens chromosome 11 clone CTC-227C10 map 11q, WORKING DRAFT
DEFINITION      SEQUENCE, 18 unordered pieces.
ACCESSION       AP001480
VERSION         AP001480.2 GI:8117338
KEYWORDS        HGC, HTGS_PHASE1, HTGS_DRAFT.
SOURCE          Homo sapiens DNA, clone CTC-227C10.
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE       1 (bases 1 to 115027)
                Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
                Fujiyama,A., Yada,T., Toriohi,Y., Watanabe,H. and Sakaki,Y.
                Homo sapiens 115,027 genomic DNA of 11q
                Published only in Database (2000)
                2 (bases 1 to 115027)
                Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
                Fujiyama,A., Yada,T., Toriohi,Y., Watanabe,H. and Sakaki,Y.
                Direct Submission
TITLE           JOURNAL
AUTHORS
REFERENCE
JOURNAL
TITL
JOURN
COMMENT
On May 30, 2000 this sequence version replaced gi:7288164.
----- Genome Center
Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgc.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: Humdraft11
Center clone name: CTC-227C10
----- Summary Statistics
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 107728 bases at least Q40
Consensus quality: 110501 bases at least Q30
Consensus quality: 111810 bases at least Q20
Insert size: 113327; sum-of-contigs
Quality coverage: 6.70x in Q20 bases; sum-of-contigs

```

NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved

```

    *
    *
    * NOTE: This is a "working draft" sequence. It currently
    * consists of 18 contigs. The true order of the pieces
    * is not known and their order in this sequence record is
    * arbitrary. Gaps between the contigs are represented as
    * runs of N, but the exact sizes of the gaps are unknown.
    * This record will be updated with the finished sequence
    * as soon as it is available and the accession number will
    * be preserved.
    *
    *
    * 1      15681: contig of 15681 bp in length
    *
    * 15682 15781: gap of 100 bp
    *
    * 15782 30275: contig of 14494 bp in length
    *
    * 30276 30375: gap of 100 bp
    *
    * 30376 40528: contig of 10153 bp in length
    *
    * 40529 40628: gap of 100 bp
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    * 40629 50205: contig of 9577 bp in length
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    * 50206 50305: gap of 100 bp
    *
    * 50306 59617: contig of 9312 bp in length
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    * 59618 59717: gap of 100 bp
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    * 59718 66750: contig of 7033 bp in length
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    * 91242 91341: gap of 100 bp
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    * 91342 96419: contig of 5078 bp in length
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    * 96420 96519: gap of 100 bp
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    * 100645 100744: gap of 100 bp
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    * 103024 105950: contig of 2927 bp in length
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    * 108939 109038: gap of 100 bp
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    * 111578 111677: gap of 100 bp
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    * 111678 113487: contig of 1810 bp in length
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    * 113488 113587: gap of 100 bp
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misc_feature	66851..73847	/note="assembly_fragment"
misc_feature	73948..77964	/note="assembly_fragment"
misc_feature	79745..85653	/note="assembly_fragment"
misc_feature	85754..91241	/note="assembly_fragment"
misc_feature	91342..96419	/note="assembly_fragment"
misc_feature	96520..100644	/note="assembly_fragment"
misc_feature	100745..102923	/note="assembly_fragment"
misc_feature	103024..105950	/note="assembly_fragment"
misc_feature	106051..108938	/note="assembly_fragment"
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Best Local Similarity	99.2%: Pred. NO. 2.5e-27;	
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Db 55154	GCATTGGGCTTGCCTCCCTCAGAGCCCTGCAGTGGAGTTCCACTTTCTCATGGG 55095	
OY 61	CAAACTTACTTGGCTCAGTCTCTGGGGCTCAGAGTCCCGGCGAGATGCTCTGG 120	
Db 55094	CAAACTTACTTGGCTCAGTCTCTGGGGCTCAGAGTCCCGGCGAGATGCTCTGG 55035	
OY 121	C 121	
Db 55034	C 55034	
RESULT 6		
AP001481/c	175582 bp	linear
LOCUS	Homo sapiens chromosome 11 clone CTC-270C21 map 11q	WORKING DRAFT
DEFINITION	SEQUENCE, 29 unordered pieces.	
ACCESSION	AP001481	
VERSION	AP001481.2	
KEYWORDS	HTG: HTGS_PHASE1; HTGS-DRAFT.	
SOURCE	Homo sapiens DNA, clone:CTC-270C21.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
TITLE	1 (bases 1 to 175582)	
JOURNAL	Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,	
REFERENCE	Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.	
AUTHORS	2 Published Only in Database (2000)	
REFERENCE	Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,	
AUTHORS	Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.	
TITLE	Direct Submission	


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misc_feature 155533..158018
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misc_feature 158119..160661
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misc_feature 165355..167624
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Query Match          99.7%; Score 120.6; DB 2; Length 175582;
Best Local Similarity 99.2%; Pred. No. 2.5e-27;
Matches 120; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGGGCTGCTCTCTCCAGAGGCCCTCGAGTGCAGTTTCCTTCATGCGG 60
    |||||||
Db 108162 GCATTGGGCTGCTCTCTCCAGAGGCCCTCGAGTGCAGTTTCCTTCATGCGG 108103

QY 61 CAAATCTYACTTTCGCTCCAGTCTCGGGGCTCAGAGTCCCTGCGCCAGATGCTCTTGC 120
    |||||||
Db 108102 CAAATCTYACTTTCGCTCCAGTCTCGGGGCTCAGAGTCCCTGCGCCAGATGCTCTTGC 108043

QY 121 C 121
Db 108042 C 108042

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RESULT 7
 AC007707/7 188971 bp DNA linear PRI 25-NOV-1999
 LOCUS Homo sapiens chromosome 11 clone 442e11 from RPC111 library map
 DEFINITION
 AC007707
 VERSION AC007707.13 GI:5764724
 KEYWORDS
 HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE
 1 (bases 1 to 188971)
 AUTHORS Shaikh, T.H., Budarf, M.L., Celis, L., Zackai, E.H. and Emanuel, B.S.
 TITLE Clustered 11q23 and 22q11 breakpoints ad 3:1 meiotic malsegregations
 in multiple unrelated t(11;22) families
 JOURNAL Am. J. Hum. Genet. (1999) In press
 REFERENCE 2 (bases 1 to 188971)
 AUTHORS Hu, P. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL

```

JOURNAL Submitted (02-JUN-1999) Department of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 3 (bases 1 to 188971)
AUTHORS Hu, P. and Roe, B.A.
TITLE Direct Submission
JOURNAL Submitted (25-AUG-1999) Department of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 4 (bases 1 to 188971)
AUTHORS Hu, P. and Roe, B.A.
TITLE Direct Submission
JOURNAL Submitted (26-AUG-1999) Department of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
REFERENCE 5 (bases 1 to 188971)
AUTHORS Hu, P. and Roe, B.A.
TITLE Direct Submission
JOURNAL Submitted (25-NOV-1999) Department of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
COMMENT On Aug 25, 1999 this sequence version replaced gi:5757506.
FEATURES
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              1..188971
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                /db_xref="taxon:9606"
                /map="11q23"
                /clone="442e11 from RPC111 library"
                /note="442e11 was originally named b1030"
BASE COUNT 53091 a 44581 c 42653 g 48646 t
ORIGIN

Query Match          99.7%; Score 120.6; DB 9; Length 188971;
Best Local Similarity 99.2%; Pred. No. 2.5e-27;
Matches 120; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGGGCTGCTCTCTCCAGAGGCCCTCGAGTGCAGTTTCCTTCATGCGG 60
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Db 78721 GCATTGGGCTGCTCTCTCCAGAGGCCCTCGAGTGCAGTTTCCTTCATGCGG 78662

QY 61 CAAATCTYACTTTCGCTCCAGTCTCGGGGCTCAGAGTCCCTGCGCCAGATGCTCTTGC 120
    |||||||
Db 78661 CAAATCTYACTTTCGCTCCAGTCTCGGGGCTCAGAGTCCCTGCGCCAGATGCTCTTGC 78602

QY 121 C 121
Db 78601 C 78601

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RESULT 8
 AC074203 42479 bp DNA linear PRI 13-OCT-2000
 LOCUS Homo sapiens chromosome 22q11 clone cos4, complete sequence.
 DEFINITION
 AC074203
 VERSION AC074203.3 GI:9625348
 KEYWORDS
 HTG.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 42479)
 AUTHORS Yang, L., Hu, P., Wu, H., Tapia-Paez, I. and Roe, B.A.
 TITLE Homo sapiens Chromosome 22q11 Cosmid cos4
 JOURNAL Unpublished
 REMARK This clone is a chimeric cosmid from a patient with t(11;22)
 translocation and it is from the derivative chromosome 11. There
 are sequences from both chromosome 11 and 22 in this cosmid
 2 (bases 1 to 42479)
 REFERENCE Yang, L., Hu, P., Wu, H., Tapia-Paez, I. and Roe, B.A.
 AUTHORS Direct Submission
 TITLE Submitted (18-JUL-2000) Department of Chemistry And Biochemistry,
 JOURNAL The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,

OK 73019, USA
 3 (bases 1 to 42479)
 Yang, L., Hu, P., Wu, H., Tapia-Paez, I. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (03-AUG-2000) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 4 (bases 1 to 42479)
 Yang, L., Hu, P., Wu, H., Tapia-Paez, I. and Roe, B.A.
 TITLE Direct Submission
 JOURNAL Submitted (13-OCT-2000) Department of Chemistry And Biochemistry,
 The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
 OK 73019, USA
 COMMENT On Aug 1, 2000 this sequence version replaced gi:9441829.
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 /db_xref="taxon:9606"
 /chromosome="22q11"
 /clone="cos4"
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 Best Local Similarity 98.3%; Pred. No. 8.1e-27;
 Matches 119; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GCATTTGGCTTGCCTCTCTCAGAGCCCTCGAGTGGAGTTTCATCTTCATGCGG 60
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 DB 31388 GCATTTGGCTTGCCTCTCTCAGAGCCCTCGAGTGGAGTTTCATCTTCATGCGG 31447
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 QY 61 CAAATCTACTTTCCTCAGTTCCTGAGGCTCAGAGTCCCTGCGCCAGATGCTCTTGC 120
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 DB 31448 CAAATCTACTTTCCTCAGTTCCTGAGGCTCAGAGTCCCTGCGCCAGATGCTCTTGC 31507
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 QY 121 C 121
 DB 31508 C 31508

RESULT 9
 AC113242 181412 bp DNA linear HTG 27-FEB-2002
 LOCUS Pan troglodytes clone RP43-68H20, WORKING DRAFT SEQUENCE, 4
 DEFINITION
 AC113242
 AC113242.1 GI:18958669
 HTG: HTGS.PHASE1: HTGS_DRAFT.
 SOURCE Pan t:oglodyles.
 ORGANISM Pan t:oglodyles
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 1 (bases 1 to 181412)
 Martin, J., Hosseini, R., Peng, Y., Peng, Z., Rubin, E.M. and Cheng, J.F.
 TITLE Direct Submission
 JOURNAL Unpublished
 2 (bases 1 to 181412)
 Martin, J., Hosseini, R., Peng, Y., Peng, Z., Rubin, E.M. and Cheng, J.F.
 TITLE Direct Submission
 JOURNAL Submitted (27-FEB-2002) Berkeley PGA, Lawrence Berkeley National
 Laboratory, 1 Cyclotron rd., Berkeley, CA 94720, United States of
 America
 COMMENT Draft Sequence Produced by Berkeley PGA
 pga.lbl.gov
 Center Code: PGABERK.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 4 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will

* be preserved.
 1 2162: contig of 2162 bp in length
 * 2163 2262: gap of unknown length
 * 2263 5105: contig of 2843 bp in length
 * 5106 5205: gap of unknown length
 * 5206 47902: contig of 42697 bp in length
 * 47903 48002: gap of unknown length
 * 48003 181412: contig of 133410 bp in length.
 FEATURES
 SOURCE Location/Qualifiers
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 /db_xref="taxon:9598"
 /clone="RP43-68H20"
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 ORIGIN
 Query Match 97.0%; Score 117.4; DB 2; Length 181412;
 Best Local Similarity 97.5%; Pred. No. 2.5e-26;
 Matches 118; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GCATTTGGCTTGCCTCTCTCAGAGCCCTCGAGTGGAGTTTCATCTTCATGCGG 60
 |||||||
 DB 102546 GCATTTGGCTTGCCTCTCTCAGAGCCCTCGAGTGGAGTTTCATCTTCATGCGG 102605
 |||||||
 QY 61 CAAATCTACTTTCCTCAGTTCCTGAGGCTCAGAGTCCCTGCGCCAGATGCTCTTGC 120
 |||||||
 DB 102606 CAAATCTACTTTCCTCAGTTCCTGAGGCTCAGAGTCCCTGCGCCAGATGCTCTTGC 102665
 |||||||
 QY 121 C 121
 DB 102666 C 102666

RESULT 10
 AC118574 191656 bp DNA linear HTG 19-APR-2002
 LOCUS Lemur catta clone LB2-277C3, WORKING DRAFT SEQUENCE, 10 unordered
 DEFINITION
 AC118574
 AC118574.1 GI:20198538
 HTG: HTGS.PHASE1: HTGS_DRAFT.
 SOURCE Lemur catta.
 ORGANISM Lemur catta.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Strepsirhini; Lemuridae; Lemur.
 1 (bases 1 to 191656)
 Martin, J., Hosseini, R., Peng, Y., Peng, Z., Rubin, E.M. and Cheng, J.F.
 TITLE Direct Submission
 JOURNAL Unpublished
 2 (bases 1 to 191656)
 Martin, J., Hosseini, R., Peng, Y., Peng, Z., Rubin, E.M. and Cheng, J.F.
 TITLE Direct Submission
 JOURNAL Submitted (19-APR-2002) Genome Sciences, Lawrence Berkeley National
 Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
 COMMENT Draft Sequence Produced by Berkeley PGA
 web site: http://pga.lbl.gov
 Center Code: PGABERK
 Additional Information:
 Comparative analysis and ordering by homology are available
 here: http://pga.lbl.gov/cgi-bin/search/cvcdtype=navalue-APOA1
 Funding agent: Programs for Genomic Applications (NHLBI)
 Contact: Jody Schwartz/ jschwartz@lbl.gov
 Summary Statistics
 Sequencing vector: Plasmid; pUC18
 Chemistry: Dye-terminator Big Dye
 Assembly program: Phrap version 0.990329.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 10 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.


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* 11111 11210: gap of unknown length
* 11211 12358: contig of 1148 bp in length
* 12359 12458: gap of unknown length
* 12459 13851: contig of 1393 bp in length
* 13852 13952: gap of unknown length
* 13952 15147: contig of 1196 bp in length
* 15148 15247: gap of unknown length
* 15248 16349: contig of 1102 bp in length
* 16350 16449: gap of unknown length
* 16450 17680: contig of 1231 bp in length
* 17681 17780: gap of unknown length
* 17781 19551: contig of 1771 bp in length
* 19552 19651: gap of unknown length
* 19652 20914: contig of 1263 bp in length
* 20915 21014: gap of unknown length
* 21015 22689: contig of 1675 bp in length
* 22690 22789: gap of unknown length
* 22790 24844: contig of 2055 bp in length
* 24845 24944: gap of unknown length
* 24945 26501: contig of 1557 bp in length
* 26502 28343: contig of 1742 bp in length
* 28344 28443: gap of unknown length
* 28444 30014: contig of 1571 bp in length
* 30015 31432: contig of 1318 bp in length
* 31433 31532: gap of unknown length
* 31533 33878: contig of 2346 bp in length
* 33879 33978: gap of unknown length
* 33979 35999: contig of 2021 bp in length
* 36000 36099: gap of unknown length
* 36100 37879: contig of 1780 bp in length
* 37880 37979: gap of unknown length
* 37980 40493: contig of 2514 bp in length
* 40494 40593: gap of unknown length
* 40594 43007: contig of 2414 bp in length
* 43008 43107: gap of unknown length
* 43108 45425: contig of 2318 bp in length
* 45426 45525: gap of unknown length
* 45526 47696: contig of 2171 bp in length
* 47697 47796: gap of unknown length
* 47797 49161: contig of 1365 bp in length
* 49162 49261: gap of unknown length
* 49262 51962: contig of 2701 bp in length
* 51963 52062: gap of unknown length
* 52063 54983: contig of 2921 bp in length
* 54984 55083: gap of unknown length
* 55084 57601: contig of 2518 bp in length
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* 57702 59300: contig of 1599 bp in length
* 59301 59400: gap of unknown length
* 59401 61170: contig of 1770 bp in length
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* 61271 63401: contig of 2131 bp in length
* 63402 63501: gap of unknown length
* 63502 66845: contig of 3344 bp in length
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* 66946 68915: contig of 1970 bp in length
* 68916 69015: gap of unknown length
* 69016 71351: contig of 2336 bp in length
* 71352 71451: gap of unknown length
* 71452 73280: contig of 1829 bp in length
* 73281 73380: gap of unknown length
* 73381 75221: contig of 3141 bp in length
* 75222 76621: gap of unknown length
* 76622 79787: contig of 3166 bp in length
* 79788 79887: gap of unknown length
* 79888 83405: contig of 3518 bp in length
* 83406 83505: gap of unknown length
* 83506 85714: contig of 2209 bp in length
* 85715 85814: gap of unknown length
* 85815 87631: contig of 1817 bp in length

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* 87632 87731: gap of unknown length
* 87732 89911: contig of 2160 bp in length
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* 91543 91642: gap of unknown length
* 91643 94772: contig of 3130 bp in length
* 94773 94872: gap of unknown length
* 94873 96801: contig of 2029 bp in length
* 96802 96902: gap of unknown length
* 96903 97001: gap of unknown length
* 97002 99943: contig of 2942 bp in length
* 99944 100043: gap of unknown length
* 100044 102874: contig of 2831 bp in length
* 102875 102974: gap of unknown length
* 102975 106306: contig of 3332 bp in length
* 106307 106406: gap of unknown length
* 106407 110217: contig of 3811 bp in length
* 110218 110317: gap of unknown length
* 110318 113346: contig of 3029 bp in length
* 113347 113446: gap of unknown length
* 113447 115933: contig of 2487 bp in length
* 115934 116033: gap of unknown length
* 116034 120425: contig of 4392 bp in length
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* 120526 123358: contig of 2833 bp in length
* 123359 123458: gap of unknown length
* 123459 126381: contig of 2923 bp in length
* 126382 126481: gap of unknown length

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Query Match 29.3%; Score 35.4; DB 2; Length 185476;
Best Local Similarity 66.2%; Pred. No. 1.5;
Matches 51; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Qy 26 GCCCTGCGAGTGGAGTTCCTTCCTGAGGCAATCTACTTGGCTCCAGTCC 85
Db 81542 GCTCTTCACAGCAATCCAGTTTCCTCATTTGGCTGAAAACGTACTAATCCAGTTCC 81601
Qy 86 TGGGGCTCAGAGTCCCT 102
Db 81602 AGGAGATCTGAACCTT 81618

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RESULT 15

AC025626

LOCUS 154696 bp DNA linear HTG 28-MAY-2000

DEFINITION

Homo sapiens clone RP11-216B13, WORKING DRAFT SEQUENCE, 35

ACCESSION

AC025626

VERSION

AC025626.3

KEYWORDS

HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

AC025626 154696 bp DNA linear HTG 28-MAY-2000

LOCUS 154696 bp DNA linear HTG 28-MAY-2000

DEFINITION Homo sapiens clone RP11-216B13, WORKING DRAFT SEQUENCE, 35

ACCESSION AC025626

VERSION AC025626.3 GI:8099800

KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 154696)

AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, F., Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choe, Y., Colangelo, M., Collins, S., Collins, A., Cooke, P., DeRubeis, K., Dewar, K., Diaz, J.S., Dodge, S., Domingo, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Glade, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heath, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lacombe, K., Lamazares, R., Landers, T., Lechoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Margulis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McNeely, R., Melnick, J., Meneses, J., Mihova, T., Miranda, C., Miñana, V., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Piatre, N.,

TITLE
JOURNAL
COMMENT

Submitted (12-MAR-2000) Whitehead Institute/MIT Center for Genome Research 320 Charles Street, Cambridge, MA 02141, USA
On May 28, 2000 this sequence version replaced g1:7657088.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIDR

Web site: http://www.seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L5807

Center clone name: 216.B.13

Summary Statistics

Sequencing vector: M13: M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 135951 bases at least Q40

Consensus quality: 145629 bases at least Q30

Consensus quality: 148984 bases at least Q20

Insert size: 149000; agarose-fp

Quality coverage: 3.7 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 35 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1088: contig of 1088 bp in length
* 1089 1188: gap of 100 bp
* 1189 2246: contig of 1058 bp in length
* 2247 2346: gap of 100 bp
* 2347 3505: contig of 1159 bp in length
* 3506 3605: gap of 100 bp
* 3606 4777: contig of 1172 bp in length
* 4778 4877: gap of 100 bp
* 4878 6634: contig of 1757 bp in length
* 6635 6734: gap of 100 bp
* 6735 8097: contig of 1363 bp in length
* 8098 8197: gap of 100 bp
* 8198 10306: contig of 2109 bp in length
* 10307 10406: gap of 100 bp
* 10407 12406: contig of 2000 bp in length
* 12407 12506: gap of 100 bp
* 12507 14219: contig of 1713 bp in length
* 14220 14319: gap of 100 bp
* 14320 16072: contig of 1753 bp in length
* 16073 16172: gap of 100 bp
* 16173 17723: contig of 1551 bp in length
* 17724 17823: gap of 100 bp
* 17824 19608: contig of 1785 bp in length
* 19609 19708: gap of 100 bp
* 19709 22007: contig of 2299 bp in length
* 22008 22107: gap of 100 bp
* 22108 23950: contig of 1843 bp in length
* 23951 24050: gap of 100 bp
* 24051 26881: contig of 2831 bp in length
* 26882 26981: gap of 100 bp
* 26982 29772: contig of 2791 bp in length
* 29773 29872: gap of 100 bp

FEATURES

source

29873 32507: contig of 2635 bp in length
* 32508 32607: gap of 100 bp
* 32608 36314: contig of 3707 bp in length
* 36315 36414: gap of 100 bp
* 36415 38838: contig of 2424 bp in length
* 38839 38938: gap of 100 bp
* 38939 42279: contig of 3341 bp in length
* 42280 42379: gap of 100 bp
* 42380 44940: contig of 2561 bp in length
* 44941 45040: gap of 100 bp
* 45041 48483: contig of 3443 bp in length
* 48484 48583: gap of 100 bp
* 48584 52752: contig of 4169 bp in length
* 52753 52852: gap of 100 bp
* 52853 57771: contig of 4919 bp in length
* 57772 57871: gap of 100 bp
* 57872 61962: contig of 4091 bp in length
* 61963 62062: gap of 100 bp
* 62063 65728: contig of 3666 bp in length
* 65729 65828: gap of 100 bp
* 65829 69752: contig of 3924 bp in length
* 69753 69852: gap of 100 bp
* 69853 76487: contig of 6635 bp in length
* 76488 76587: gap of 100 bp
* 76588 84995: contig of 8408 bp in length
* 84996 85095: gap of 100 bp
* 85096 91863: contig of 6768 bp in length
* 91864 91963: gap of 100 bp
* 91964 104501: contig of 12538 bp in length
* 104502 104601: gap of 100 bp
* 104602 116857: contig of 12256 bp in length
* 116858 116957: gap of 100 bp
* 116958 127000: contig of 10043 bp in length
* 127001 127100: gap of 100 bp
* 127101 140329: contig of 13229 bp in length
* 140330 140429: gap of 100 bp
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/clone_id="RPC1-11 Human Male BAC"
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1189. 2246
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2347. 3505
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3606. 4777
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10407. 12406
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12507. 14219
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14320. 16072
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16173. 17723
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17824. 19608
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19709. 22007
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24051. 26881
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misc_feature      29673.    .32507
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misc_feature      32608.    .35314
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misc_feature      38939.    .42279
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misc_feature      45041.    .48483
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misc_feature      48584.    .52752
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Query Match	28.9%	Score 35;	DB 2;	Length 154696;
Best Local Similarity	55.6%	Pred. No. 2.1;		
Matches	65;	Conservative	1;	Mismatches 51; Indels 0; Gaps 0;

[illegible]

Search completed: November 21, 2002, 03:10:02
Job time : 3494 secs


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FT conflict
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FT
XX WO200100803-A2.
XX 04-JAN-2001.
XX PD 21-JUN-2000; 2000WO-IB01011.
XX PF

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XX 25-JUN-1999; 99US-0141032.
PR 20-DEC-1999; 99WO-1B02058.
PR 21-DEC-1999; 99US-0469099.
XX
PA (GEST ) GENSET.
XX
PI Yen F, Denison B, Bour B, Bihain B, Bougueleret L, Duclert A;
PI Dunas Milne Edwards J;
XX WPI: 2001-071485/08.
XX
PT Nucleic acids encoding apolipoprotein A-IV-related proteins (AA4RP) and
PT biallelic markers of AA4RP, useful for diagnosing lipid metabolism
PT related disorders and/or liver related disorders -
XX
PS Claim 3; Page 242-244; 260pp; English.
XX
CC The present sequence is that of an alternative genomic sequence
CC (see also AAF30035) of human apolipoprotein A-IV-related protein
CC (AA4RP). It encodes a 366-amino acid protein (see AAB20103). AA4RP
CC is differentially expressed in obese mouse models, indicating a role
CC in lipid metabolism related disorders. It appears to be the human
CC homologue of rat regeneration associated protein (RAP3), which is
CC believed to be involved in liver regeneration, and is likely to
CC have a similar function. It also shows 52% similarity to
CC apolipoprotein A-IV, and is likely to have a similar function. The
CC invention also provides AA4RP cDNAs (see AAF30036) and polypeptides,
CC biallelic markers identified in the AA4RP gene and from genomic
CC regions flanking the gene, and methods for genotyping a nucleic
CC acid containing 1 or more of the biallelic markers. Also provided
CC is a method for detecting a statistical correlation between a
CC biallelic marker allele and a phenotype and/or between a biallelic
CC marker haplotype and a phenotype. Diagnostic methods are provided
CC for determining whether an individual is at risk of developing a
CC lipid metabolism related disorder and/or a liver related disorder,
CC such as obesity, diabetes or coronary heart disease, and whether
CC the individual suffers from such a disorder as a result of a
CC polymorphism in the AA4RP gene. AA4RP DNA constructs can be
CC used to direct temporal and spatial AA4RP gene expression in
CC recombinant cell hosts and in transgenic animals. They can also
CC be used for recombinant production of AA4RP polypeptides, and as
CC probes and primers.
XX
SQ Sequence 5381 BP; 1104 A; 1434 C; 1709 G; 1132 T; 2 other;

```

```

Query Match 99.7%; Score 120.6; DB 22; Length 5381;
Best Local Similarity 100.0%; Pred. No. 8e-29;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

OY 1 GCATTGGGCTTGCCTCTCAGAGGCCCTCGAGTGGAGTTACGCTTTCTCATGGG 60
DB 252 GCATTGGGCTTGCCTCTCAGAGGCCCTCGAGTGGAGTTACGCTTTCTCATGGG 311
OY 61 CAAATCTYACTTTCGCTCAGTTCCTGCGGCGACAGTCCCTGGGCCAGATGCCCTTGC 120
DB 312 CAAATCTYACTTTCGCTCAGTTCCTGCGGCGACAGTCCCTGGGCCAGATGCCCTTGC 371
OY 121 C 121
DB 372 C 372

```

```

RESULT 2
AAF30035
ID AAF30035 standard; DNA; 81001 BP.
AC AAF30035;
XX 23-APR-2001 (first entry)
XX Human apolipoprotein A-IV-related protein (AA4RP) gene.
XX DE
XX

```


	misc_binding	77046..77070
FT	/+lag- at	
FT	/note= *20-853-415 probe*	
XX		
PN	MO200100803-A2.	
PD		
XX	04-JAN-2001.	
PF	21-JUN-2000; 2000MO-IBO1011.	
XX		
PR	25-JUN-1999; 99US-0141032.	
PR	20-DEC-1999; 99WO-IBO2058.	
PR	21-DEC-1999; 99US-0469099.	
PA	(GEST) GENSET.	
PI		
P1	Yen F, Denison B, Bour B, Bihain B, Bougueleret L, Duclert A;	
XX	Dumas MLine Edwards J;	
DR	WPI: 2001-071485/08.	
DR	P-PSDB; AAB20103.	
PT	Nucleic acids encoding apolipoprotein A-IV-related proteins (AA4Rp) and	
XX	biallelic markers of AA4Rp, useful for diagnosing lipid metabolism	
XX	related disorders and/or liver related disorders -	
PS	Claim 1; Page 216-238; 260bp; English.	
CC	The present sequence is that of the human apolipoprotein	
CC	A-IV-related protein (AA4Rp) gene on chromosome 11. The gene	
CC	encodes a 366-amino acid protein (see AAB20103). AA4Rp is	
CC	differentially expressed in obese mouse models, indicating a role	
CC	in lipid metabolism related disorders. It appears to be the human	
CC	homologue of rat regeneration associated protein (RAP3), which is	
CC	believed to be involved in liver regeneration, and is likely to	
CC	have a similar function. It also shows 52% similarity to	
CC	apolipoprotein A-IV, and is likely to have a similar function. The	
CC	invention also provides AA4Rp cDNAs (see AAF30036) and polypeptides,	
CC	biallelic markers identified in the AA4Rp gene and from genomic	
CC	regions flanking the gene, and methods for genotyping a nucleic	
CC	acid containing 1 or more of the biallelic markers. Also provided	
CC	is a method for detecting a statistical correlation between a	
CC	biallelic marker allele and a phenotype and/or between a biallelic	
CC	marker haplotype and a phenotype. Diagnostic methods are provided	
CC	for determining whether an individual is at risk of developing a	
CC	lipid metabolism related disorder and/or a liver related disorder,	
Query Match	99.7%; Score 120.6; DB 22; Length 81001;	
Best Local Similarity	100.0%; Pred. No. 1.8e-28;	
Matches 121; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 GCATTTGGGCTTGCCTCCTCAAGAGGCCCGCACATGACATTTCCTCATGGCG 60	
Db	12280 GCATTTGCGCTGTCTCTCTCGAAGGCCCTGGAGAGTTCAGCTTTCCTCATGGCG 12339	
OY	61 CAAATCTACTTTCGCTCAGTTCCGCGGGGCTCAGAGTCCCGGGCCCAATGCTCTTGC 120	
Db	12340 CAAATCTACTTTCGCTCAGTTCTCGGGGCTCAGAGTCCCGGGCCCAATGCTCTTGC 12399	
OY	121 C 121	
Db	12400 C 12400	
RESULT 3		
ID	ABK28380/c	
XX	ABK28380 standard; DNA: 5377 BP.	
AC	ABK28380;	
DT	23-APR-2002 (first entry)	
DE	DNA transcription associated complementary genomic DNA #127.	

XX	DNA transcription associated gene: peptide nucleic acid; PNA-oligomer;
KW	PNA: cytosine methylation state; SNP: retroviral infection; gene: ds;
KW	single nucleotide polymorphism; adenosine deaminase deficiency; cancer;
KW	viral infection; Sezary syndrome; haematological disorder; tuberculosis;
KW	immunological disorder; Werner syndrome; developmental disorder;
KW	psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis;
KW	neurodegenerative disorder; Waardenburg syndrome; Niemann-Pick disease;
KW	myelodysplastic syndrome; myocardial infarction; hypertension; arthritis;
KW	angiogenesis; congenital heart disease; HDR syndrome; gene therapy;
KW	polyglutamine disorder; solid tumour.
XX	
OS	unidentified.
XX	
PN	WO2001/92565-A2.
XX	
PD	06-DEC-2001.
XX	
PF	06-APR-2001; 2001WO-EP03973.
XX	
PR	06-APR-2000; 2000DE-1019058.
XX	07-APR-2000; 2000DE-1019173.
PR	30-JUN-2000; 2000DE-1032529.
XX	
PR	01-SEP-2000; 2000DE-1043826.
XX	
PA	(EPIG-) EPIGENOMICS AG.
XX	
PI	Olek A, Plepenbrock C, Berlin K;
DR	WPI: 2002-090046/12.
XX	
PT	New nucleic acids or oligomers, useful for diagnosing or treating
PT	diseases associated with DNA transcription, e.g. immunological
PT	tumours, Werner syndrome, psoriasis, myocardial infarction, solid
PT	tumours or cancer -
XX	
PS	Claim 1; SEQ ID No 254; 32pp; English.
XX	
XX	The invention relates to a nucleic acid, which comprises a segment of the
CC	chemically pretreated DNA of genes associated with DNA transcription from
CC	one of 346 sequences, and an oligomer, in particular an oligonucleotide
CC	or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical
CC	to the chemically pretreated DNA of genes associated with DNA
CC	transcription. The set of oligomer probes are useful for detecting the
CC	cytosine methylation state and/or single nucleotide polymorphisms (SNPs)
CC	in a chemically pretreated genomic DNA. The nucleic acids are useful for
CC	diagnosing or treating diseases associated with DNA transcription
CC	(particularly with the methylation status), e.g. adenosine deaminase
CC	deficiency, viral infection, retroviral infection, Sezary syndrome,
CC	haematological disorders, immunological disorders, Werner syndrome,
CC	neurological disorders, developmental disorders, psoriasis, Rieger's syndrome,
CC	neurological disorders, neurodegenerative disorders, Waardenburg
CC	syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial
CC	infarction, hypertension, angiogenesis, erythropoiesis, congenital heart
CC	disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours
CC	or cancer. Sequences ABX28127-ABX28472 represent DNA transcription
CC	associated genomic DNA molecules of the invention.
CC	Note: The sequence data for this patent did not form part of the printed
CC	specification but was obtained in electronic format directly from the
CC	European Patent Office.
XX	
SO	Sequence 5377 BP: 1117 A; 176 C; 1481 G; 2603 T; 0 other;
	Query Match 44.1%; Score 53.4; DB 24; Length 5377;
	Best Local Similarity 77.8%; Fred. No. 3.1e-07;
	Matches 63; Conservative 1; Mismatches 17; Indels 0; Gaps 0;
QY	41 TTACACTTTTCTCCATGCGGCAATCTACTTCCCTCCAGTTCCTGGGCTCAGAGTCC 100
	:
DB	5376 TTCAACTTTTCTCTCAATAAACAATCTCACTTCCCTCCAAATTCCTAAACTCAAAATCC 5317
QY	101 CTGGCCCAAGATGCTCTTGCC 121

PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSEQ-) HYSEQ INC.
XX
PI Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI: 2001-44253/47.
DR P-PSDB: AAM39607.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
PS Claim 1; SEQ ID NO 966; 10078bp; English.
XX
CC The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 3446 BP; 759 A; 991 C; 1094 G; 602 T; 0 other;
XX
Query Match 24.3%; Score 29.4; DB 22; Length 3446;
Best Local Similarity 55.7%; Pred. No. 14;
Matches 54; Conservative 1; Mismatches 42; Indels 0; Gaps 0;
XX
QY 7 GGGCTGCTCTCTCTCAGAGGCGCTGAGTGCAGCTTTTCTTCATGGGCAATC 66
DB 2319 GTGCTACTGCTGCTCCCAAGGCGCTTCCAGACTTTTCCACGTTGCTGCTGCGACATG 2260
QY 67 TTAATTGCTGCTCCAGTCTCTGCGGCGCTCAGAGTCCCTG 103
DB 2259 ACACAAATCTCTCCGCTCCGAGGCGCAAGCTCCCG 2223
XX
RESULT 8
AAK70514/c
ID AAK70514 standard; DNA; 12730 BP.
XX
AC AAK70514;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:25526.
XX
KW Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;
KW cytosstatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.

XX
PF 17-JAN-2001; 2001MO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-MAR-2000; 2000US-0198123.
PR 19-MAR-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225278.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
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PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.

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PR 29-SEP-2000: 2000US-0236369.
PR 29-SEP-2000: 2000US-0236370.
PR 02-OCT-2000: 2000US-0236802.
PR 02-OCT-2000: 2000US-0237037.
PR 02-OCT-2000: 2000US-0237038.
PR 02-OCT-2000: 2000US-0237039.
PR 02-OCT-2000: 2000US-0237040.
PR 13-OCT-2000: 2000US-0239935.
PR 13-OCT-2000: 2000US-0239937.
PR 20-OCT-2000: 2000US-0240960.
PR 20-OCT-2000: 2000US-0241221.
PR 20-OCT-2000: 2000US-0241785.
PR 20-OCT-2000: 2000US-0241786.
PR 20-OCT-2000: 2000US-0241787.
PR 20-OCT-2000: 2000US-0241809.
PR 20-OCT-2000: 2000US-0241809.
PR 01-NOV-2000: 2000US-0241826.
PR 08-NOV-2000: 2000US-0244617.
PR 08-NOV-2000: 2000US-0246474.
PR 08-NOV-2000: 2000US-0246475.
PR 08-NOV-2000: 2000US-0246476.
PR 08-NOV-2000: 2000US-0246477.
PR 08-NOV-2000: 2000US-0246478.
PR 08-NOV-2000: 2000US-0246523.
PR 08-NOV-2000: 2000US-0246524.
PR 08-NOV-2000: 2000US-0246525.
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PR 08-NOV-2000: 2000US-0246527.
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PR 08-NOV-2000: 2000US-0246609.
PR 08-NOV-2000: 2000US-0246610.
PR 08-NOV-2000: 2000US-0246611.
PR 08-NOV-2000: 2000US-0246613.
PR 17-NOV-2000: 2000US-0249207.
PR 17-NOV-2000: 2000US-0249208.
PR 17-NOV-2000: 2000US-0249209.
PR 17-NOV-2000: 2000US-0249210.
PR 17-NOV-2000: 2000US-0249211.
PR 17-NOV-2000: 2000US-0249212.
PR 17-NOV-2000: 2000US-0249213.
PR 17-NOV-2000: 2000US-0249214.
PR 17-NOV-2000: 2000US-0249215.
PR 17-NOV-2000: 2000US-0249216.
PR 17-NOV-2000: 2000US-0249217.
PR 17-NOV-2000: 2000US-0249218.
PR 17-NOV-2000: 2000US-0249244.
PR 17-NOV-2000: 2000US-0249245.
PR 17-NOV-2000: 2000US-0249264.
PR 17-NOV-2000: 2000US-0249265.
PR 17-NOV-2000: 2000US-0249297.
PR 17-NOV-2000: 2000US-0249299.
PR 17-NOV-2000: 2000US-0249300.
PR 01-DEC-2000: 2000US-0250160.
PR 01-DEC-2000: 2000US-0250391.
PR 05-DEC-2000: 2000US-0251030.
PR 05-DEC-2000: 2000US-0251988.
PR 05-DEC-2000: 2000US-0251988.
PR 06-DEC-2000: 2000US-0251479.
PR 08-DEC-2000: 2000US-0251856.
PR 08-DEC-2000: 2000US-0251868.
PR 08-DEC-2000: 2000US-0251869.
PR 08-DEC-2000: 2000US-0251989.
PR 08-DEC-2000: 2000US-0251990.
PR 11-DEC-2000: 2000US-0254097.
PR 05-JAN-2001: 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM,
XX
XX MPI: 2001-483426/52.
XX

```

```

PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
PS
PS Disclosure: SEQ ID NO 25326; 3071bp + Sequence Listing: English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (1)
CC amino acid sequences given in AAK62170 to AAK91921. (1) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (1)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (1) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (1) by expressing inactive proteins or to
CC supplement the patient's own production of (1). Additionally, (1)
CC polynucleotides may be used to produce the secreted (1), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (1) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 12730 BP; 2891 A; 3333 C; 3652 G; 2854 T; 0 other:
Query Match 24.3%; Score 29.4; DB 22; Length 12730;
Best Local Similarity 55.7%; Pred. No. 20;
Matches 54; Conservative 1; Mismatches 42; Indels 0; Gaps 0;
QY 7 GGGCTTGCTCTCTCAGAGCCCTGGAGTGAGTTCAGTTCCTCATGGGCAATC 66
DB 1999 GTGCTTACCTGCTCTCCCAAGGCCCTTCACACTTTTTCACCTGCTCTGTCGCACATG 1940
QY 67 TTAGCTTGCTCTCAGTTCCTGGGGCTCAGATCCCG 103
DB 1939 ACACAATCTCTCCGCTCCGAGGAGCCAGCTCCCG 1903
AC AAX99032
AC AAX99032;
XX
XX AAX99032 standard; cDNA; 845 BP.
XX
DT 24-SEP-1999 (first entry)
XX
XX Human validated cancer cell derived cDNA #354.
DE
XX
XX Cancer: human; colon; breast; lung; transmembrane receptor; ATPase;
XX integral membrane protein; aspartyl protease; GATA family; wnt family;
XX transcription factor; G-protein alpha subunit; protein phosphatase;
XX photolabile binding protein; diacylglycerol binding protein; tyrosin;
XX protein kinase; tyrosine phosphatase; developmental signalling protein;
XX WW/rsp5/GMP domain; therapy; forensic; genetic mapping; diagnostic;
XX detection; treatment; cervical; melanoma; colorectal adenocarcinoma;
XX Wilms' tumour; retinoblastoma; sarcoma; myosarcoma; lung carcinoma;
XX leukemia; lymphoma; dysplasia; hyperplasia; endometrium; adrenal;
XX prostate; ss.
XX
XX Homo sapiens.
XX
XX MO9933982-A2.
XX
XX 08-JUL-1999.
XX
XX 22-DEC-1998; 98WO-US27610.
XX
XX 21-DEC-1998; 98US-0217471.
XX 23-DEC-1997; 97US-0068755.
XX 03-APR-1998; 98US-0080664.
XX 21-OCT-1998; 98US-0105234.
XX 27-OCT-1998; 98US-0105877.
XX

```

XX (CHIR) CHIRON CORP.
 PA (HYSR-) HYSEQ INC.
 XX
 PI Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
 PI Escobedo J, Garcia PD, Garcia V, Glese K, Innis MA;
 PI Jones LW, Kassam A, Kennedy GC, Kita D, Labat I;
 PI Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
 PI Stache-Crain B, Sudduth-Klinger J, Williams LT;
 XX
 DR WPI: 1999-430243/36.
 XX
 PT New isolated human polynucleotides
 XX
 PS Claim 1: Page 555; 591pp; English.
 XX
 CC This invention describes novel isolated human polynucleotides obtained
 CC by screening for differential expression in colon cancer, breast cancer
 CC and lung cancer cell lines. The polynucleotides of the invention are
 CC represented in MAY98275-X99118 and encode polypeptides of protein
 CC families selected from 4 transmembrane segments integral membrane
 CC proteins, 7 transmembrane receptors, ATPases associated with various
 CC cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of
 CC transcription factors, G-protein alpha subunit, phospholipase or
 CC diacylglycerol binding proteins, protein kinase, protein phosphatase 2C,
 CC protein tyrosine phosphatase, trypsin, wnt family of developmental
 CC signaling proteins and WW/Trsp5/MWP domain containing proteins. The
 CC encoded polypeptides also have a functional domain selected from Ank
 CC repeat, basic region plus leucine zipper transcription factors,
 CC bromodomain, EF-hand, SH3 domain, WD domain/G-beta repeats, zinc finger
 CC (C2H2 type), zinc finger (CCHC class), and zinc-binding metalloprotease
 CC domain. The polynucleotides encode polypeptides with similarity to known
 CC protein families and are predicted to have similar properties. The novel
 CC polynucleotides can be used to develop products for use as therapeutic
 CC agents and in forensics, genetic analysis, mapping and diagnostic
 CC applications. In particular, the product can be used for the detection
 CC and management of cancers. They can be used for treating e.g. cervical
 CC cancers, melanomas, colorectal adenocarcinomas, Wilms' tumour, sarcomas,
 CC retinoblastoma, myosarcomas, lung carcinomas, leukemias, such as chronic
 CC myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and
 CC myeloid leukemia, and lymphomas such as histiocytic lymphoma, anhydritic
 CC hereditary ectodermal dysplasia, congenital alveolar dysplasia,
 CC epithelial dysplasia of the cervix, fibrous dysplasia of bone, and
 CC mammary dysplasia, hyperplasias, e.g. endometrial, adrenal, breast,
 CC prostate or thyroid hyperplasias or pseudoeplitheliomatous hyperplasia of
 CC the skin.
 XX
 SQ Sequence 845 BP; 215 A; 144 C; 170 G; 236 T; 80 other;
 XX
 Query Match 24.1%; Score 29.2; DB 20; Length 845;
 Best Local Similarity 53.8%; Pred. No. 11;
 Matches 49; Conservative 1; Mismatches 41; Indels 0; Gaps 0;
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 QY 1 GCATTGGGCTTGCTCTCCAGAGAGCCCTGGCAGTGGAGTTGCTTTCTCATGGG 60
 Db 74 GCNTGGGCGCTTGGGCGCTGAGGAGCGGTGAGGCTTACGCTTACGCTTACGCGC 133
 OY 61 CAAATCTTACTTGGCTGCTGAGTTCCTGGGGC 91
 Db 134 AAAAAGCTGCACGACGACACANTTCCGCTTNC 164
 XX
 RESULT 10
 ID AAL04978 standard; DNA; 1768 BP.
 XX
 AC AAL04978;
 XX
 DT 21-NOV-2001 (first entry)
 XX
 DE Human reproductive system related antigen DNA SEQ ID NO: 7666.
 XX
 KW Human; reproductive system related antigen; reproductive system disorder;

KW cancer; gene therapy; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200155320-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01339.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
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PR	08-NOV-2000	2000US-0246526	2000US-0246526
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PR	17-NOV-2000	2000US-0249209	2000US-0249209
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PR	17-NOV-2000	2000US-0249213	2000US-0249213
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PR	17-NOV-2000	2000US-0249216	2000US-0249216
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PR	17-NOV-2000	2000US-0249246	2000US-0249246
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PR	17-NOV-2000	2000US-0249267	2000US-0249267
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PR	05-DEC-2000	2000US-0256119	2000US-0256119
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PR	11-DEC-2000	2000US-0254097	2000US-0254097
PR	05-JAN-2001	2001US-0259678	2001US-0259678

xx (HUMA-) HUMAN GENOME SCI INC.
 PA
 xx
 PI Rosen CA, Barash SC, Ruben SM;
 xx
 DR WPI: 2001-465570/50.
 xx
 PT Isolated nucleic acid molecule encoding a reproductive system antigen
 PT is used in preventing, treating or ameliorating a medical condition
 xx
 PS Disclosure: SEQ ID NO 7666; 1297pp + Sequence Listing; English.
 xx
 CC The present invention provides the protein and coding sequences of a
 CC number of human reproductive system related antigens. These can be used
 CC in the prevention and treatment of reproductive system disorders,
 CC including cancer. The present sequence is a genomic sequence encoding a
 CC protein of the invention.
 CC
 SQ Sequence 1768 BP; 445 A; 440 C; 461 G; 422 T; 0 other:

Query Match	23.8%	Score 28.8	DB 22	Length 1768
Best Local Similarity	55.1%	Pred. No. 18		
Matches 54	Conservative 1	Mismatches 43	Indels 0	Gaps 0

QY	12	TGCTGTCACAGAGCCCTGGCGATGAGATTACGCTTTTCCATGAGGGCAACTCTACT	71
Db	1100	TGCTATTGTCAAAATGCTGTGAAAGACAGTTGTCCCTTTACCTTTAGGAGAGAGGCTCCT	1159
QY	72	TTGCGTCCAGTTCCTGGGGCTCAGAGTCCCTGACCCAG	109
Db	1160	TACACTGACATTCAAAAGTCTTCAATGACCCGCCCCAC	1197

XX	RESULT 11
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ID	AA104979 standard; DNA: 1768 BP.
XX	
AC	AA104979;
XX	
DT	21-NOV-2001 (first entry)
XX	
DE	Human reproductive system related antigen DNA Seq ID NO: 7667.
XX	
XX	Human; reproductive system related antigen; reproductive system disorder;
KM	Cancer; gene therapy; ds.
XX	
OS	Homo sapiens.
XX	
PN	WO200155320-A2.
XX	
PD	02-AUG-2001.
XX	
XX	
PF	17-JAN-2001; 2001WO-0501339.
XX	
PR	31-JAN-2000; 2000US-0179065.
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PR	28-JUN-2000; 2000US-0214886.
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 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA Rosen CA, Barash SC, Ruben SM;
 PI WPI; 2001-465570/50.
 DR
 XX
 XX Isolated nucleic acid molecule encoding a reproductive system antigen
 PT is used in preventing, treating or ameliorating a medical condition -
 XX
 XX
 PS Disclosure; SEQ ID NO 7667; 1297bp + Sequence listing; English.
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 CC in the prevention and treatment of reproductive system disorders,
 CC including cancer. The present sequence is a genomic sequence encoding a
 CC protein of the invention.
 XX
 SQ Sequence 1768 BP; 445 A; 441 C; 459 G; 422 T; 1 other;
 Query Match 23.8%; Score 28.8; DB 22; Length 1768;
 Best Local Similarity 55.1%; Pred. No. 18;
 Matches 54; Conservative 1; Mismatches 43; Indels 0; Gaps 0;
 QY 12 TGCCTCTCTAGAGAGCCCTGCGATGAGTTCACCTTTCTCTATGAGGCAATCTTACT 71
 Db 1100 TCGATTGTCAAAATGTCGTAAGACAAAGTGTCTTACCTTACCTTAGAGAGAGGCTCT 1159
 QY 72 TTGCTCCAGTCTCTGGGCTCAGAGTCCCTGGCCAG 109

Db 1160 TACACTGACATTCAAAGTCTCATGACCCGCCCCAG 1197

RESULT 12

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ID ABL97871 standard; DNA: 1768 BP.

XX ABL97871:

AC 21-JUN-2002 (first entry)

XX Human testicular antigen encoding DNA fragment SPQ ID NO: 2523.

XX Human; testicular antigen; testes; cancer; metastasis; immune disorder;

KM reproductive system disorder; urinary system disorder; gene therapy;

KM cardiovascular disorder; respiratory disorder; neurological disorder;

KM gastrointestinal disease; infection; cytostatic; gene; ds.

XX OS Homo sapiens.

XX PN WO20015317-A2.

XX PD 02-AUG-2001.

XX PF 17-JAN-2001; 2001WO-US01329.

XX PR 31-JAN-2000; 2000US-0179065.

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PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
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PR 08-NOV-2000; 2000US-0246611.
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PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
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PR 17-NOV-2000; 2000US-0249264.

PR 29-SEP-2000; 2000US-0236370.
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 PR 05-DEC-2000; 2000US-0251031.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0255719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251858.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251899.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0253978.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Rosen CA, Barash SC, Ruben SM;
 XX WPI: 2001-483232/52.
 XX
 PT Nucleic acids encoding 973 human testicular antigen polypeptides,

PT useful for preventing, diagnosing and/or treating testicular cancer
 XX
 XX Disclosure: SEQ ID NO 2524; 766pp: English.
 PS
 XX The present invention provides the protein and coding sequences of 973
 CC human testicular antigens, and fragments of their genomic sequences. The
 CC sequences can be used in the treatment of cardiovascular, urinary system,
 CC reproductive system, immune, respiratory, neurological and
 CC gastrointestinal disorders, infections, and particularly cancer,
 CC especially testicular cancers. The present sequence is a DNA encoding a
 CC protein fragment of the invention.
 XX
 SQ Sequence 1768 BP; 445 A; 441 C; 459 G; 422 T; 1 other:
 Query Match 23.8%; Score 28.8; DB 23; Length 1768;
 Best Local Similarity 35.1%; Pred. No. 18;
 Matches 54; Conservative 1; Mismatches 43; Indels 0; Gaps 0;
 OY 12 TGCCTCCTCAGAGCGCCGAGTGAGTTCAGCTTTCTCCTCAGGCAATCTACT 71
 DB 1100 TCGTATGTGCAATGTGCTGAAAGACAACTTCTCCTTACCTTAGCAGAGCGCTCT 1159
 OY 72 TTGCTCCAGTTCCTGGGCTCAGAGTCCCTGCCAC 109
 DB 1160 TACACTGACATTCAAAGTCTCAATGACCGGCCAC 1197
 RESULF 14
 ABNS9848
 ID ABNS9848 standard; cDNA: 3549 BP.
 XX
 AC ABNS9848:
 XX
 DT 28-JUN-2002 (first entry)
 XX
 DE Novel human coding sequence SEQ ID NO: 259.
 XX
 XX Human; antihaemic; vulnery; antiinflammatory; immunomodulator;
 KM antifertility; cerebroprotective; cytostatic; rheumatic; gene therapy;
 KM neuroprotective; antiparkinsonian; protein therapy; EST;
 KM expressed sequence tag; gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200222660-A2.
 XX
 XX 21-MAR-2002.
 XX
 PF 10-SEP-2001; 2001WO-US26015.
 XX
 XX 11-SEP-2000; 2000US-0659671.
 PR
 XX (HYSE-) HYSEQ INC.
 PA
 PI Tang YF, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Wehrman T, Drmanac RT.
 PI WPI: 2002-292408/33.
 DR P-PSDB: ABB97435.
 XX
 PT An isolated polynucleotide for treating diseases associated with its
 encoded polypeptide such as cancer and multiple sclerosis -
 XX
 PS Claim 1: SEQ ID NO 259; 509pp: English.
 XX
 CC The present invention provides the protein and coding sequences of 444
 CC novel human proteins. These were isolated from expressed sequences tags
 CC (ESTs). They can be used to stimulate cell growth, to regulate
 CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
 CC e.g. in burn treatment, to regulate the immune system e.g. to treat
 CC multiple sclerosis, to regulate activin or inhibin e.g. to treat
 CC infertility, to regulate haemostasis or thrombolysis e.g. to treat
 CC stroke and cancer, to screen for drugs, to treat inflammatory conditions

CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
 CC Parkinson's disease. The present sequence is a coding sequence of the
 CC invention.

XX Sequence 3549 BP; 767 A; 1007 C; 991 G; 784 T; 0 other;

Query Match 23.6%; Score 28.6; DB 24; Length 3549;
 Best Local Similarity 59.7%; Pred. No. 25;
 Matches 46; Conservative 1; Mismatches 30; Indels 0; Gaps 0;

QY 37 GCAGTTCACCTTTCCATGCGGCAAACTCTTCCGCTCCAGTTCGGGCTCAGA 96
 111 11111 1111 11111 : 1 111 11 11111 11
 DB 1010 GCATGTACAGCTTCAGCTCCGCAAACTCCCACTGAGACCACTTTCTGGGCTGCAG 1069

OY 97 GTCCCTGGCCAGATGC 113
 11 1111 111 111
 DB 1070 GTTCTGCACCACTGC 1086

RESULT 15

AAC74939
 ID AAC74939 standard; cDNA: 4224 BP.

XX AAC74939;

DE 08-FEB-2001 (first entry)

XX Human ORFX ORF494 polynucleotide sequence SEQ ID NO:987.

XX Human: open reading frame; ORFX; detection; cytostatic; hepatotropic;
 XX vulnary; antiparkinsonian; antiparkinsonian; nootropic; neuroprotective;
 XX anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 XX immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 XX hypotensive; dermatological; immunosuppressive; antineoplastic;
 XX antiviral; antibacterial; antifungal; antineoplastic; antihypertensive;
 XX antianemic; gene therapy; cancer; proliferative disorder; hypertension;
 XX neurodegenerative disorder; osteoarthritis; graft vs host disease;
 XX cholesterolester storage; diabetes mellitus; hypothyroidism; SCID; AIDS;
 XX severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 XX allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 XX bone damage; cartilage damage; antiinflammatory disease; coagulation;
 XX thrombosis; contraceptive; ss.

XX Homo sapiens.

XX WO200058473-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US08621.

XX 31-MAR-1999; 99US-0127607.

XX 02-APR-1999; 99US-0127636.

XX 05-APR-1999; 99US-0127728.

XX 30-MAR-2000; 2000US-0540763.

XX (CURA-) CURAGEN CORP.

XX Shinketsu RA, Leach M;

XX WPI; 2000-602362/57.

XX P-PSDB; AAB40730.

XX Novel nucleic acids and peptides derived from open reading frame X,
 XX useful for treating e.g. cancers, proliferative disorders,
 XX neurodegenerative disorders and cardiovascular disease -

XX Claim 5; Page 962-964; 5507pp; English.

XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 XX which represent the human ORFX open reading frames 1 to 3161. The ORFX
 XX sequences have activities such as: cytostatic; hepatotropic; vulnary;

CC antiparkinsonian; nootropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antineoplastic; antibacterial; antiviral; antineoplastic; antineoplastic;
 CC antihypertensive; antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 4224 BP; 961 A; 1150 C; 1123 G; 988 T; 2 other;

Query Match 23.6%; Score 28.6; DB 21; Length 4224;
 Best Local Similarity 59.7%; Pred. No. 26;
 Matches 46; Conservative 1; Mismatches 30; Indels 0; Gaps 0;

OY 37 GCAGTTCACCTTTCCATGCGGCAAACTCTTCCGCTCCAGTTCGGGCTCAGA 96
 111 11111 1111 11111 : 1 111 11 11111 11
 DB 1488 GCATGTACAGCTTCAGCTCCGCAAACTCCCACTGAGACCACTTTCTGGGCTGCAG 1547

OY 97 GTCCCTGGCCAGATGC 113
 11 1111 111 111
 DB 1548 GTTCTGCACCACTGC 1564

Search completed: November 21, 2002, 02:11:55
 Job time : 311 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 21, 2002, 01:57:53 : Search time 2185 Seconds
(without alignments)
896.867 Million cell updates/sec

Title: US-09-842-364-1_COPY_12280_12400

Sequence: 1 gcatlgtggtctctcctccl.....tgcgcagatgctcttgc 121

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: em_estba:*
2: em_estlum:*
3: em_estlin:*
4: em_estmu:*
5: em_estrov:*
6: em_estropl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl1:*
10: gb_estl2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vtl:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	33.2	27.4	448	12	BF724998 bx10h11.y
C 3	33.2	27.4	457	13	BG982886 PMO-CN015
C 4	33.2	27.4	573	10	BE252183 601113780
C 5	33.2	27.4	692	10	BE256387 601117848
C 6	33.2	27.4	698	10	AW793634 MRI-DM000

C 7	33.2	27.4	787	12	BG744224
C 8	33.2	27.4	812	13	AL528119
C 9	33.2	27.4	832	13	BM019314 603647443
C 10	33.2	27.4	872	14	B0896139 AGNCOURT
C 11	33.2	27.4	938	9	AL520679
C 12	33.2	27.4	979	9	AL560785
C 13	33.2	27.4	984	9	AL560022
C 14	33.2	27.4	986	9	AL556053
C 15	33.2	27.4	996	9	AL583065
C 16	33.2	27.4	1007	12	BG762959
C 17	33.2	27.4	1203	12	BF795030 602256150
C 18	33.2	27.4	1203	12	BF795030 602256150
C 19	33.2	27.4	1203	12	BF795030 602256150
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C 25	33.2	27.4	1203	12	BF795030 602256150
C 26	33.2	27.4	1203	12	BF795030 602256150
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ALIGNMENTS

RESULT 1
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LOCUS MR4-HN0065-210201-004-a05 HN0065 Homo sapiens CDNA, mRNA sequence.
DEFINITION B1004187
ACCESSION B1004187
VERSION B1004187.1 GI:14408261
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brites,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
MEDLINE
COMMENT
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

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DA
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/lab_host="EMD10b"
/notes="Organ: Eye; Vector: PCWMSPORTE; Post-mortem Iris
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/notes="Organ: colon_normal; Vector: puc18; Site_1: Sma1; Site_2: Sma1; A mini-library was made by cloning products

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KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryotes: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
AUTHORS	Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
TITLE	1 (bases 1 to 938)
JOURNAL	Li, W. B., Gruber, C., Jesse, J., and Polayes, D.
COMMENT	Full-length cDNA libraries and normalization
	Unpublished (2001)
	Contact: Genoscope

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Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
FEATURES
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/lab_host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifestech.com URL :
http://fulllength.invitrogen.com"

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Query Match	27.4%	Score 33.27	DB 9	Length 938
Best Local Similarity	61.6%	Pred. No. 4.5		
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			Gaps 0	
QY	36	tgagattcagctttttccattggggcaaatcttaccttgcgcagttccctgggctgag	95	
DB	801	tggggctctctttttctttttcttttgcgttcaaatccacacttctcttccctttggagacactct	860	
QY	96	actccctggagccacatgcctctttggc	121	
DB	861	ggggccttgaggtgcctcctatggcc	886	

RESULT 12	979 bp	mRNA	linear	EST 16-FEB-2001
AL560785/c				
LOCUS	AL560785	LTI-NFLO10_BC2	Homo sapiens	cdna clone CS0DL004YA13 5
DEFINITION	prlme, mRNA sequence.			

VERSION	AL560785.1
KEYWORDS	GI:12907581
SOURCE	EST.
ORGANISM	human. Homo sapiens

REFERENCE	1,1 (bases 1 to 979)
AUTHORS	I. W. B. Gruber, C. J. Jesse, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segreff@genoscope.cns.fr, Web : www.genoscope.cns.fr

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FEATURES
SOURCE
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1. 979
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BASE COUNT      232 a      300 c      280 g      165 t      2 others
ORIGIN

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Query Match	27.4%	Score 33.2	DB 9	Length 979
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Oy	96	AGTCCCTGGCCAGATGCCCTTGGCC	121	
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RESULT 13	AL560022/c	984 nt	mRNA	linear	EST 16-FEB-2001
LOCUS	AL560022/c				
DEFINITION	AL560022 LTL.FL011_BCl Homo sapiens CDNA clone CSDG004IN06 5 prime				
ACCESSION	AL560022				
VERSION	AL560022.1				
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	1 (bases 1 to 984)				
TITLE	Li, W.B., Gruber, C., Jesse, J., and Polayes, D.				
JOURNAL	Full-length cDNA libraries and normalization				
COMMENT	Unpublished (2001)				
	Contact: Genoscope				

FEATURES	Location/Qualifiers
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BASE COUNT
ORIGIN

232 a 291 c 283 g 175 t 3 others

/note="Vector: pcMVSPORT 6: 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen, 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : liangell@lifetech.com URL : <http://fulllength.invitrogen.com>"

Query Match	27.4%	Score 33.2	DB 9	Length 984
Best Local Similarity	61.6%	Pred No. 4.6		
Matches 33, Conservative	0	Mismatches 33	Indels 0	Gaps 0

NAME/KEY: exon

LOCATION: 2243..3940
OTHER INFORMATION: exon 4
NAME/KEY: misc.feature
LOCATION: 3941..5381
OTHER INFORMATION: 3' regulatory region
NAME/KEY: allele
LOCATION: 319
OTHER INFORMATION: 17-42-319 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 3213
OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: conflict
LOCATION: 1241
OTHER INFORMATION: 17-39-343 : T in ref genbank AC007707
NAME/KEY: conflict
LOCATION: 1447
OTHER INFORMATION: 17-40-202 : G in ref genbank AC007707
NAME/KEY: primer_bind
LOCATION: 1..11022
OTHER INFORMATION: 17-42.rp
NAME/KEY: primer_bind
LOCATION: 553..11575
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer_bind
LOCATION: 899..11920
OTHER INFORMATION: 17-39.pu
NAME/KEY: primer_bind
LOCATION: 1246..12267
OTHER INFORMATION: 17-40.pu
NAME/KEY: primer_bind
LOCATION: 1441..12461
OTHER INFORMATION: 17-39.rp complement
NAME/KEY: primer_bind
LOCATION: 1632..12651
OTHER INFORMATION: 17-40.rp complement
NAME/KEY: primer_bind
LOCATION: 2964..13984
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 3432..14454
OTHER INFORMATION: 17-41.rp complement
NAME/KEY: primer_bind
LOCATION: 300..318
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 320..338
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 3194..3212
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
LOCATION: 3214..3232
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: misc.binding
LOCATION: 307..331
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc.binding
LOCATION: 3201..3225
OTHER INFORMATION: 17-41-250.probe
US-09-750-580-4

Query Match 99.7% Score 120.6; DB 4; Length 5381;
Best Local Similarity 100.0%; Pred. No. 2e-30;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCATTTGGGCTTCCTCCAGAGCCCTGCAGTGCAGTTCCAGCTTTCTCATGGG 60
DB 252 GCATTTGGGCTTCCTCCAGAGCCCTGCAGTGCAGTTCTTCATGGG 311
OY 61 CAAATCTACTTTCCTCCAGTTCCTGGGGCTCAGAGTCCCTGGCCCAATGCTTTCG 120
DB 312 CAAATCTACTTTCCTCCAGTTCCTGGGGCTCAGAGTCCCTGGCCCAATGCTTTCG 371

OY 121 C 121
DB 372 C 372

RESULT 2
US-09-750-580-1
Sequence 1, Application US/09750580
Patent No. 645280
GENERAL INFORMATION:
APPLICANT: Yen, Frances
APPLICANT: Denison, Blake
APPLICANT: Bour, Barbara
APPLICANT: Bihain, Bernard
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Duclert, Aymeric
APPLICANT: Bouguetel, Lydia
APPLICANT: Ebdets-Reed, Dana
APPLICANT: Salter-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89 US2 CIP
CURRENT APPLICATION NUMBER: US/09/750,580
PRIORITY FILING DATE: 2000-12-28
PRIORITY FILING DATE: 2000-06-21
PRIORITY FILING DATE: 2000-06-21
PRIORITY FILING DATE: 2000-06-21
PRIORITY FILING DATE: 2000-06-21
PRIORITY FILING DATE: 1999-12-20
PRIORITY FILING DATE: 1999-12-20
PRIORITY FILING DATE: 1999-12-21
PRIORITY FILING DATE: 1998-12-22
PRIORITY FILING DATE: 1998-12-22
PRIORITY FILING DATE: 1999-06-25
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 81001
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: 10946..12946
OTHER INFORMATION: 5' regulatory region
NAME/KEY: exon
LOCATION: 12947..12958
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 13470..13526
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 13641..13752
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 14271..15968
OTHER INFORMATION: exon 4
NAME/KEY: misc.feature
LOCATION: 15969..17969
OTHER INFORMATION: 3' regulatory region
NAME/KEY: allele
LOCATION: 1239
OTHER INFORMATION: 20-828-311 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12347
OTHER INFORMATION: 17-42-319 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 15241
OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 42218
OTHER INFORMATION: 20-841-149 : polymorphic base A or G
NAME/KEY: allele

LOCATION: 45442
OTHER INFORMATION: 20-842-115 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 77058
OTHER INFORMATION: 20-853-415 : polymorphic base C or T
NAME/KEY: primer_bind
LOCATION: 929..949
OTHER INFORMATION: 20-828.pu
NAME/KEY: primer_bind
LOCATION: 1357..1377
OTHER INFORMATION: 20-828.fp complement
NAME/KEY: primer_bind
LOCATION: 12029..12050
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer_bind
LOCATION: 12581..12603
OTHER INFORMATION: 17-42.fp complement
NAME/KEY: primer_bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer_bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.fp complement
NAME/KEY: primer_bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-841.pu
NAME/KEY: primer_bind
LOCATION: 42572..42591
OTHER INFORMATION: 20-841.fp complement
NAME/KEY: primer_bind
LOCATION: 45328..45347
OTHER INFORMATION: 20-842.pu
NAME/KEY: primer_bind
LOCATION: 45863..45883
OTHER INFORMATION: 20-842.fp complement
NAME/KEY: primer_bind
LOCATION: 76644..76664
OTHER INFORMATION: 20-853.pu
NAME/KEY: primer_bind
LOCATION: 77166..77185
OTHER INFORMATION: 20-853.fp complement
NAME/KEY: primer_bind
LOCATION: 1220..1238
OTHER INFORMATION: 20-828-311.mis
NAME/KEY: primer_bind
LOCATION: 1240..1258
OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer_bind
LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 12348..12366
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer_bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer_bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
NAME/KEY: primer_bind
LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer_bind
LOCATION: 77039..77057

OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc_bind
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc_bind
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_bind
LOCATION: 15229..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc_bind
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe
NAME/KEY: misc_bind
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc_bind
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-750-580-1

Query Match 99.7%; Score 120.6; DB 4; Length 81001;
Best Local Similarity 100.0%; Pred. No. 4; 7e-30;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCATTGGGCTGCTCTCTCAGAGCCCTGGAGTGAAGTTCAGTTTCTCATGGGG 60
DB 12280 GCATTGGGCTGCTCTCTCAGAGCCCTGGAGTGAAGTTCAGTTTCTCATGGGG 12339
QY 61 CAATCTYACTTTCGCTCAGTTCCTGGGGCTCAGAGTCCCTGGCCAGATGCTTTCG 120
DB 12340 CAATCTYACTTTCGCTCAGTTCCTGGGGCTCAGAGTCCCTGGCCAGATGCTTTCG 12399

QY 121 C 121
DB 12400 C 12400

RESULT 3
US-09-245-041-5/c
; Sequence 5, Application US/09245041
; Patent No. 6274339
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
; FILE REFERENCE: 7853-136
; CURRENT APPLICATION NUMBER: US/09/245,041
; EARLIER FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/093,630
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: 60/104,978
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 90050
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-245-041-5

Query Match 22.3%; Score 27; DB 4; Length 90050;
Best Local Similarity 57.8%; Pred. No. 25;
Matches 48; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 21 CAGAGCCCTCGCAGTGAAGTTCAGTTTCTCATGGGCAATCTYACTTTCGCTCA 80
DB 33058 CAGAGCCCTCGCAGTTCATTCAGCAGCTCAAGGCAAGCTGTCTAATCA 32999

QY 81 GTCTGCTGCTGAGTCCCTG 103
 Db 32998 GTCCAGGAGTCTGATCCAG 32976

RESULT 4

US-09-342-681C-8/c
 : Sequence 8, Application US/09342681C
 : Patent No. 6355782
 : GENERAL INFORMATION:
 : APPLICANT: Zonana et al.
 : TITLE OF INVENTION: Hypohydrotic ectodermal dysplasia genes and proteins
 : FILE REFERENCE: 52978
 : CURRENT APPLICATION NUMBER: US/09/342,681C
 : PRIOR FILING DATE: 1999-06-29
 : PRIOR APPLICATION NUMBER: 60/092,279
 : PRIOR FILING DATE: 1998-07-09
 : PRIOR APPLICATION NUMBER: 60/112,366
 : NUMBER OF SEQ ID NOS: 123
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 8
 : LENGTH: 977
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : US-09-342-681C-8

Query Match 22.1%; Score 26.8; DB 4; Length 977;
 Best Local Similarity 55.7%; Pred. No. 6.8;
 Matches 49; Conservative 1; Mismatches 38; Indels 0; Gaps 0;

QY 10 CTGCTCTCTCAGAGCCCTGCGAGTGTGAGTTCCTTCATGGGCAATCTYA 69
 Db 524 CCTTTCCTCCCTACCTCAGCAGTGTGTGTGAGCCATGCTCCCTGCAAGCCCTG 465
 QY 70 CTGCTCAGTCTCTGCGGCTGAG 97
 Db 464 TGTAGCTTTATTCTCCAGGCTGAG 437

RESULT 5

US-09-097-319A-19/c
 : Sequence 19, Application US/09097319A
 : Patent No. 6384207
 : GENERAL INFORMATION:
 : APPLICANT: Ainley, Michael
 : APPLICANT: Armstrong, Katherine
 : APPLICANT: Belmar, Scott
 : APPLICANT: Folkerts, Otto
 : APPLICANT: Hopkins, Nicole
 : APPLICANT: Menke, Michael A.
 : APPLICANT: Parredy, Dayakar
 : APPLICANT: Petolino, Joseph P.
 : APPLICANT: Smith, Kelley
 : APPLICANT: Woosley, Aaron
 : TITLE OF INVENTION: Regulatory Sequences for Transgenic Plants
 : NUMBER OF SEQUENCES: 59
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Dowling Patent Department
 : STREET: 9330 Zionsville Road
 : CITY: Indianapolis
 : STATE: Indiana
 : COUNTRY: USA
 : ZIP: 46268
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/097,319A
 : FILING DATE:
 : CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:
 : NAME: Stuart, Donald R.
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 317 337 4816
 : TELEFAX: 317 337 4847
 : INFORMATION FOR SEQ ID NO: 19:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 9335 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: circular
 : MOLECULE TYPE: DNA
 : US-09-097-319A-19

Query Match

22.1%; Score 26.8; DB 4; Length 9335;
 Best Local Similarity 52.7%; Pred. No. 14;
 Matches 58; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 8 GGCTGCTCTCTCAGAGCCCTGCGAGTGTGAGTTCCTTCATGGGCAATCT 67
 Db 5920 GCGATGTCGCTGCGGCGAGCGCGGATGTCGCGCGGCTGCTGCGGCGATGCT 5861
 QY 68 YACTTCGCTCAGTTCCTGCGGCTCAGACTCCCTGCGGCAATGCTCT 117
 Db 5860 GAATGCTTATCCGCTGCTGGAACAAATGCCCCAGATCCGCGAGCT 5811

RESULT 6

US-09-173-300-52/c
 : Sequence 52, Application US/09173300
 : Patent No. 6451581
 : GENERAL INFORMATION:
 : APPLICANT: Falco, Saverio Carl
 : APPLICANT: Hiltz, William D.
 : APPLICANT: Kinney, Anthony J.
 : APPLICANT: Cahoon, Rebecca E.
 : APPLICANT: Rafalski, J. Antoni
 : TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC ENZYMES
 : FILE REFERENCE: BB-1126
 : CURRENT APPLICATION NUMBER: US/09/173,300
 : CURRENT FILING DATE: 1998-10-15
 : EARLIER APPLICATION NUMBER: 60/063,423
 : EARLIER FILING DATE: 1997 October 28
 : NUMBER OF SEQ ID NOS: 54
 : SOFTWARE: Microsoft Word Version 7.0A
 : SEQ ID NO 52
 : LENGTH: 995
 : TYPE: DNA
 : ORGANISM: Trifolium aestivum
 : US-09-173-300-52

Query Match 22.0%; Score 26.6; DB 4; Length 995;
 Best Local Similarity 64.4%; Pred. No. 8;
 Matches 38; Conservative 1; Mismatches 20; Indels 0; Gaps 0;

QY 10 CTGCTCTCTCAGAGCCCTGCGAGTGTGAGTTCCTTCATGGGCAATCTY 68
 Db 778 CTTCATCTCCGACAGGCTGCGCTGCTAAGCTGATCTTCCCTCATGACGACCTTTC 720

RESULT 7

US-08-583-562B-9
 : Sequence 9, Application US/08583562B
 : Patent No. 5922570
 : GENERAL INFORMATION:
 : APPLICANT: Staunton, Donald
 : APPLICANT: Harris, Edith
 : TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
 : NUMBER OF SEQUENCES: 36
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
 : STREET: 233 South Wacker Drive, 6300 Sears Tower

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,562B
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/33033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-0448
TELEFAX: 312-474-6300
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1125 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1125
US-08-583-562B-9

Query Match 21.8%; Score 26.4; DB 2; Length 1125;
Best Local Similarity 60.0%; Pred. No. 9.7;
Matches 42; Conservative 1; Mismatches 27; Indels 0; Gaps 0;

QY 18 CCTCAGAGCCCTGCGAGTTCACCTTTCTCATGCGGCAATCTYACTTTCGCT 77
DB 354 CCCCTGCGCGCTGTGACTGAGCGAGATTGTGCCCATGGCAAGACTCACACTCGCT 413
QY 78 CCACTTCCTG 87
DB 414 CCGGTTTGTG 423

RESULT 8
US-08-779-113-9
Sequence 9, Application US/08779113
Patent No. 5948891
GENERAL INFORMATION:
APPLICANT: Staunton, Donald E.
APPLICANT: Harris, Edith S.
TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
TITLE OF INVENTION: Binding
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,113
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Greta E. No. 5948891and

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33773
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1125 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1125
US-08-779-113-9

Query Match 21.8%; Score 26.4; DB 2; Length 1125;
Best Local Similarity 60.0%; Pred. No. 9.7;
Matches 42; Conservative 1; Mismatches 27; Indels 0; Gaps 0;

QY 18 CCTCAGAGCCCTGCGAGTTCACCTTTCTCATGCGGCAATCTYACTTTCGCT 77
DB 354 CCCCTGCGCGCTGTGACTGAGCGAGATTGTGCCCATGGCAAGACTCACACTCGCT 413
QY 78 CCACTTCCTG 87
DB 414 CCGGTTTGTG 423

RESULT 9
US-08-583-562B-11
Sequence 11, Application US/08583562B
Patent No. 5922570
GENERAL INFORMATION:
APPLICANT: Staunton, Donald
APPLICANT: Harris, Edith
TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
TITLE OF INVENTION: Binding
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/583,562B
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27866/33033
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-0448
TELEFAX: 312-474-6300
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1494 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1449

COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,113
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Greta E. No. 594891and
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/33773
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2574 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2574
US-08-779-113-1

Query Match 21.8%; Score 26.4; DB 2; Length 2574;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 42; Conservative 1; Mismatches 27; Indels 0; Gaps 0;

QY 18 CCTCAGAGCCCTGGAGAGGAGTTCAGCTTTCATGCGGCAAACTVACTTTCGCT 77
DB 1170 CCCCTCTGGCCCTGACTGAGCAGACATGTGCCATGGGAAAGACTCACACTGCCG 1229

QY 78 CCAAGTTCCTG 87
DB 1230 CCGGTTTGTG 1239

RESULT 13
US-08-724-394A-20
Sequence 20, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Krommal, Gregory S.
APPLICANT: Laufer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A. 35,136
REGISTRATION NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 246240 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc-feature
LOCATION: 1..246240
OTHER INFORMATION: /note="HLA-H.CONFIG"
US-08-724-394A-20

Query Match 21.8%; Score 26.4; DB 2; Length 246240;
Best Local Similarity 60.0%; Pred. No. 52;
Matches 42; Conservative 1; Mismatches 27; Indels 0; Gaps 0;

QY 37 GGAGTTCACTTTCTCCTGAGGCAAACTVACTTTCGCTCAGTTCCTGGGCTCAGA 96
DB 160999 GGCCTTCGCCCTATTCTTCTTGCGCGCCGCTTCTAGAGCTTGACAACTTGCGCTTGGC 161058

QY 97 GTCCCTGGCC 106
DB 161059 GGCCTTGGCC 161068

RESULT 14
US-08-724-394A-21
Sequence 21, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Krommal, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Laufer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereto
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 21:

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? SEQUENCE CHARACTERISTICS:
?     LENGTH: 246240 base pairs
?     type: nucleic acid
?     STRANDEDNESS: not relevant
?     TOPOLOGY: not relevant
?     MOLECULE TYPE: cDNA
?     FEATURE:
?         NAME/KEY: misc_feature
?         LOCATION: 1..246240
?         OTHER INFORMATION: /note= "HLA-H. CONTIG
US-08-724-394A-21

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Query Match	21.8%	Score 26.4	DB 2	Length 246240
Best Local Similarity	60.0%	Pred. No. 52		
Matches 42	Conservative 1	Mismatches 27	Indels 0	Gaps 0

Oy 37 GGAATTCAGCTTTTCCATCGGGGCAAACTTACTTTCCGTCCAGTTCTGGGCCTACA 96
|| ||| | | | | : | | | | | || ||||| |
Db 160999 GGCGTTCGCTATTCTTCTGGGGCGGCCCTTCTTAAGGCTTGACACACTTGCGCTTAGC 161058

```
QY      97  GTCCCTGGCC 106
          | | | | |
Db 161059 GGCCTTGGGC 161068
```

RESULT 15
US-08-724-394A-22
; Sequence 22, Application US/08724394A

1
2
3
4
5
6
7
8
9
10
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? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.00, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/06/724,394A

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1  FILING DATE: 01-OCT-1996
2  CLASSIFICATION: 536
3  ATTORNEY/AGENT INFORMATION:
4  NAME: Fitts, Renee A.
5  REGISTRATION NUMBER: 35,136
6  REFERENCE/DOCKET NUMBER: 017957-000100
7  TELECOMMUNICATION INFORMATION:
8  TELEPHONE: 415-576-0200
9  TELEFAX: 415-576-0300
10 INFORMATION FOR SEO ID NO: 22:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 246240 base pairs
13 TYPE: nucleic acid
14 STRANDEDNESS: not relevant
15 TOPOLOGY: not relevant
16 MOLECULE TYPE: cDNA
17 FEATURE:
18 NAME/KEY: misc_feature
19 LOCATION: 1..246240

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OTHER INFORMATION: /note- "HLA-H. CONTIG"
US-08-724-394A-22

Query Match	21.8%	Score 26.4;	DB 2;	Length 246240;
Best Local Similarity	60.0%;	Pred. No. 52;		
Matches 42;	Conservative 1;	Mismatches 27;	Indels 0;	Gaps 0;

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Db 160999 GGCCTTGCCCTATTTCYTCTTTGGCGGCCCTTCYTAGGCTTGACAACTTGGCCTTACG 161058

QY 97 GTCCCTGGCC 106
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Db 161059 GGCCCTGGCC 161068

Search completed: November 21, 2002, 03:45:50
Job time : 280 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2002, 02:06:48 ; Search time 82 Seconds
(without alignments)
558,858 Million cell updates/sec

Title: US-09-842-364-1_COPY_12280_12400

Sequence: 1 gcattggcgtctctctc.....tgcacagatcctctgc 121

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 335578 seqs, 18936513 residues

Total number of hits satisfying chosen parameters: 671156

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: /cgn2_6/pdatata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	120.6	99.7	81001	10	US-09-751-877-1
3	120.6	99.7	3117	10	US-09-728-446-405
4	120.6	99.7	504	10	US-09-783-590-5953
5	120.6	99.7	1026	10	US-09-886-055-28
6	120.6	99.7	1091	9	US-10-011-597-1
7	120.6	99.7	3000	10	US-09-919-172-13
8	120.6	99.7	222	10	US-09-783-590-11626
9	120.6	99.7	524	10	US-09-864-761-15294
10	120.6	99.7	524	10	US-09-864-761-15294
11	120.6	99.7	4926	10	US-09-893-238-5
12	120.6	99.7	1147	10	US-09-789-561-57
13	120.6	99.7	15980	10	US-09-764-864-1714
14	120.6	99.7	472	10	US-09-864-761-5516
15	120.6	99.7	494	10	US-09-917-800A-61
16	120.6	99.7	995	12	US-10-027-450-53
17	120.6	99.7	341	10	US-09-764-864-538
18	120.6	99.7	389	10	US-09-864-761-25624
19	120.6	99.7	522	10	US-09-864-761-8963

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21	26.4	21.8	1391	10	US-09-880-107-3740	Sequence 3740, App
22	26.4	21.8	5607	9	US-10-109-605-92	Sequence 92, App1
23	26.4	21.8	1138	10	US-09-778-844-165	Sequence 165, App
24	26.4	21.8	1137	10	US-09-778-844-164	Sequence 164, App
25	26.4	21.8	1137	10	US-09-778-844-166	Sequence 166, App
26	26.4	21.8	1206	12	US-10-062-254-145	Sequence 143, App
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41	26.4	21.8	720	10	US-09-815-242-9471	Sequence 9471, App
42	26.4	21.8	261	9	US-09-728-444-1027	Sequence 1027, App
43	26.4	21.8	1632	9	US-09-887-381-3	Sequence 3, App1
44	26.4	21.8	1827	10	US-09-974-288-174	Sequence 174, App
45	26.4	21.8	1827	10	US-09-919-172-48	Sequence 48, App1

ALIGNMENTS

RESULT 1
US-09-751-877-4
Sequence 4, Application US/09751877
Patent No. US20020142949A1
GENERAL INFORMATION:
APPLICANT: Yen, Frances
APPLICANT: Denison, Blake
APPLICANT: Bour, Barbara
APPLICANT: Dumais, Milne Edwards, Jean-Baptiste
APPLICANT: Dunclet, Aymeric
APPLICANT: Bouguetel, Lydie
APPLICANT: Bouguetel, Lydie
APPLICANT: Bouguetel, Lydie
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89, US3, PRC
CURRENT FILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent, pm
SEQ ID NO 4
LENGTH: 5381
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: 1..918
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
LOCATION: 919..930
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 1442..1498
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 1613..1724
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 2243..3940
OTHER INFORMATION: exon 4
NAME/KEY: misc.feature
LOCATION: 3941..5361

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OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 319
OTHER INFORMATION: 17-42-319 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 3213
OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: conflict
LOCATION: 1241
OTHER INFORMATION: 17-39-343 : T in ref genbank AC007707
NAME/KEY: conflict
LOCATION: 1447
OTHER INFORMATION: 17-40-202 : G in ref genbank AC007707
NAME/KEY: primer_bind
LOCATION: 1..11022
OTHER INFORMATION: 17-42-.pu
NAME/KEY: primer_bind
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LOCATION: 899..11920
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LOCATION: 300..318
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NAME/KEY: primer_bind
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LOCATION: 307..331
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_binding
LOCATION: 3201..3225
OTHER INFORMATION: 17-41-250.probe
US-09-751-877-4

Query Match          99.7%; Score 120.6; DB 10; Length 5381;
Best Local Similarity 100.0%; Pred. No. 9.3e-31;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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US-09-751-877-1
Sequence 1. Application US/09751877
Patent No. US20020142949A1
GENERAL INFORMATION:
APPLICANT: Yen, Frances
APPLICANT: Denison, Blake
APPLICANT: Bour, Barbara
APPLICANT: Bihain, Bernard
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Boucleret, Lydie
APPLICANT: Ebbets-Reed, Dana
APPLICANT: Salter-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC CELL GROWTH
FILE REFERENCE: 89 US3 REG
CURRENT APPLICATION NUMBER: US/09/751,877
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 81001
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 10946..12946
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
LOCATION: 12947..12958
OTHER INFORMATION: exon 1
NAME/KEY: exon
LOCATION: 13470..13526
OTHER INFORMATION: exon 2
NAME/KEY: exon
LOCATION: 13641..13752
OTHER INFORMATION: exon 3
NAME/KEY: exon
LOCATION: 14271..15968
OTHER INFORMATION: exon 4
NAME/KEY: misc_feature
LOCATION: 15969..17969
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1239
OTHER INFORMATION: 20-828-311 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 12347
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NAME/KEY: allele
LOCATION: 15241
OTHER INFORMATION: 17-41-250 : polymorphic base C or T
NAME/KEY: allele
LOCATION: 42218
OTHER INFORMATION: 20-841-149 : polymorphic base A or G
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LOCATION: 45442
OTHER INFORMATION: 20-842-115 : polymorphic base A or G
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LOCATION: 77058
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NAME/KEY: primer_bind
LOCATION: 12581..12603
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OTHER INFORMATION: 17-42-TP complement
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LOCATION: 45328..45347
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NAME/KEY: primer_bind
LOCATION: 45863..45883
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OTHER INFORMATION: 20-853-pu
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LOCATION: 77166..77185
OTHER INFORMATION: 20-853-TP complement
NAME/KEY: primer_bind
LOCATION: 1220..1238
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NAME/KEY: primer_bind
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OTHER INFORMATION: 20-828-311.mis complement
NAME/KEY: primer_bind
LOCATION: 12328..12346
OTHER INFORMATION: 17-42-319.mis
NAME/KEY: primer_bind
LOCATION: 12348..12366
OTHER INFORMATION: 17-42-319.mis complement
NAME/KEY: primer_bind
LOCATION: 15222..15240
OTHER INFORMATION: 17-41-250.mis
NAME/KEY: primer_bind
LOCATION: 15242..15260
OTHER INFORMATION: 17-41-250.mis complement
NAME/KEY: primer_bind
LOCATION: 42199..42217
OTHER INFORMATION: 20-841-149.mis
NAME/KEY: primer_bind
LOCATION: 42219..42237
OTHER INFORMATION: 20-841-149.mis complement
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LOCATION: 45423..45441
OTHER INFORMATION: 20-842-115.mis
NAME/KEY: primer_bind
LOCATION: 45443..45461
OTHER INFORMATION: 20-842-115.mis complement
NAME/KEY: primer_bind
LOCATION: 77039..77057
OTHER INFORMATION: 20-853-415.mis
NAME/KEY: primer_bind
LOCATION: 77059..77077
OTHER INFORMATION: 20-853-415.mis complement
NAME/KEY: misc_binding
LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
NAME/KEY: misc_binding
LOCATION: 12335..12359
OTHER INFORMATION: 17-42-319.probe
NAME/KEY: misc_binding
LOCATION: 15228..15253
OTHER INFORMATION: 17-41-250.probe
NAME/KEY: misc_binding
LOCATION: 42206..42230
OTHER INFORMATION: 20-841-149.probe

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NAME/KEY: misc_binding
LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
NAME/KEY: misc_binding
LOCATION: 77046..77070
OTHER INFORMATION: 20-853-415.probe
US-09-751-877-1
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Best Local Similarity 99.7%; Score 120.6; DB 10; Length 81001;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCATTGGCCCTCTCTCTCAGAGCCCTCCGAGTCAGCTTTCCTCATGGCG 60
DB 12280 GCATTGGCCCTCTCTCTCAGAGCCCTCCGAGTCAGCTTTCCTCATGGCG 12339
QY 61 CAAATCTYACTTTCGCTCCAGTTCCTGGGCTCAGAGTCCCTGGCCAGATGCCCTTTCG 120
DB 12340 CAAATCTYACTTTCGCTCCAGTTCCTGGGCTCAGAGTCCCTGGCCAGATGCCCTTTCG 12399
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DB 12400 C 12400

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RESULT 3
US-09-728-446-405
Sequence 405, Application US/09728446
Patent No. US20020081668A1
GENERAL INFORMATION:
APPLICANT: Friedlich, Glenn
APPLICANT: Zambrowicz, Brian
TITLE OF INVENTION: No. US20020081668A1 Murine Polynucleotide Sequences
FILE REFERENCE: LEX-0101-USA
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,270
NUMBER OF SEQ ID NOS: 1461
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 405
LENGTH: 317
TYPE: DNA
ORGANISM: Mus musculus
US-09-728-446-405
Query Match
Best Local Similarity 25.5%; Score 30.8; DB 10; Length 317;
Matches 53; Conservative 0; Mismatches 37; Indels 0; Gaps 0;
QY 20 TCAGAGGCCCTCGAGTTCAGCTTTCATGAGCAATCTYACTTTCGCTCC 79
DB 167 TCAGAGGCCCTCGAGTTCAGCTTTCATGAGCAATCTYACTTTCGCTCC 226
QY 80 AGTTCCTGGGCTCAGAGTTCGCTCCAGAGTTCGCTCCAG 109
DB 227 AGTTCAGAGGAATGACACCTTGAGAG 256

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RESULT 4
US-09-783-590-5953
Sequence 5953, Application US/09783590
Patent No. US20020110850A1
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Haodong
APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16-2C1

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1 NAME/KEY: misc feature
2 LOCATION: (288)
3 OTHER INFORMATION: n equals a,t,g, or c
4 NAME/KEY: misc feature
5 LOCATION: (303)
6 OTHER INFORMATION: n equals a,t,g, or c
7 NAME/KEY: misc feature
8 LOCATION: (364)
9 OTHER INFORMATION: n equals a,t,g, or c
10 NAME/KEY: misc feature
11 LOCATION: (399)
12 OTHER INFORMATION: n equals a,t,g, or c
13 NAME/KEY: misc feature
14 LOCATION: (403)
15 OTHER INFORMATION: n equals a,t,g, or c
16 NAME/KEY: misc feature
17 LOCATION: (406)
18 OTHER INFORMATION: n equals a,t,g, or c
19 NAME/KEY: misc feature
20 LOCATION: (421)
21 OTHER INFORMATION: n equals a,t,g, or c
22 NAME/KEY: misc feature
23 LOCATION: (422)
24 OTHER INFORMATION: n equals a,t,g, or c
25 NAME/KEY: misc feature
26 LOCATION: (424)
27 OTHER INFORMATION: n equals a,t,g, or c
28 NAME/KEY: misc feature
29 LOCATION: (427)
30 OTHER INFORMATION: n equals a,t,g, or c
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32 LOCATION: (429)
33 OTHER INFORMATION: n equals a,t,g, or c
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35 LOCATION: (433)
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37 NAME/KEY: misc feature
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39 OTHER INFORMATION: n equals a,t,g, or c
40 NAME/KEY: misc feature
41 LOCATION: (443)
42 OTHER INFORMATION: n equals a,t,g, or c
43 NAME/KEY: misc feature
44 LOCATION: (456)
45 OTHER INFORMATION: n equals a,t,g, or c
46 NAME/KEY: misc feature
47 LOCATION: (457)
48 OTHER INFORMATION: n equals a,t,g, or c
49 NAME/KEY: misc feature
50 LOCATION: (461)
51 OTHER INFORMATION: n equals a,t,g, or c
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53 LOCATION: (462)
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56 LOCATION: (470)
57 OTHER INFORMATION: n equals a,t,g, or c
58 NAME/KEY: misc feature
59 LOCATION: (486)
60 OTHER INFORMATION: n equals a,t,g, or c
61 NAME/KEY: misc feature
62 LOCATION: (496)
63 OTHER INFORMATION: n equals a,t,g, or c
64 US-09-783-590-5953
65
66 Query Match 23.0%; Score 27.8; DB 10; Length 504;
67 Best Local Similarity 57.1%; Pred. No. 2.9;
68 Matches 44; Conservative 1; Mismatches 32; Indels 0; Gaps 0;
69
70 22 AAGAGCCCTGGAGATGGAGATTCACCTTTTCATCATGGGCGCAATCTVACTTGGCTCAG 81
71 1111111111111111111111111111111111111111111111111111111111
72 165 AAGCGCCTGGAGGCTTGGAGTCCACATGCGTCCAGGGGTACACGCTCTCTGTTCGCG 224

```



```
APPLICANT: Moore, K.
APPLICANT: Nagle, D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
FILE REFERENCE: 7853-237
CURRENT FILING DATE: 2001-06-27
CURRENT APPLICATION NUMBER: US/09/893,238
PRIOR FILING DATE: 1999-07-05
PRIOR APPLICATION NUMBER: 60/093,630
PRIOR FILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: 60/104,978
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 90050
TYPE: DNA
ORGANISM: Mus musculus
US-09-893-238-5
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Query Match 22.3% Score 27; DB 10; Length 90050;
Best Local Similarity 57.8%; Pred. No. 29;
Matches 48; Conservative 0; Mismatches 35; Indels 0; Gaps 0;
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QY 21 CAGAGCCCTCGCAGTGTGAGTTCCTTCATATGGGCAATCTACTTTCCTCCCA 80
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Db 33058 CAGAGGACCTGGTTCATATCTCAGACACCTACGACGCTCAAGCTGTAAATCCA 32999
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QY 81 GTTCCTGGGGCTCAGAGTCCCTG 103
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Db 32998 GTCCAGGGGATCTGATGCCAG 32976
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RESULT 12
US-09-789-561-57/C
Sequence 57, Application US/09789561
Patent No. US20020064818A1
GENERAL INFORMATION:
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APPLICANT: NI et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: P2043P1
CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 57
LENGTH: 1147
TYPE: DNA
ORGANISM: Homo sapiens
US-09-789-561-57
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Query Match 22.1% Score 26.8; DB 10; Length 1147;
Best Local Similarity 73.9%; Pred. No. 8.3;
Matches 34; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
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QY 71 TTTCGTCAGTTCCTGGGGCTCAGAGTCCCTGGCCCAAGATGCTC 116
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Db 911 TTTCCTCAGATTATTGCCCCAGAGTCCCTGACCTGATGCTC 866
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RESULT 13
US-09-764-864-1714/C
Sequence 1714, Application US/09764864
Patent No. US20020132753A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT23
CURRENT APPLICATION NUMBER: US/09/764,864
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PAM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1714
LENGTH: 15980
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (2577)
OTHER INFORMATION: n equals a,t,g, or c
US-09-764-864-1714
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Query Match 22.1% Score 26.8; DB 10; Length 15980;
Best Local Similarity 59.7%; Pred. No. 19;
Matches 43; Conservative 1; Mismatches 28; Indels 0; Gaps 0;
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QY 40 GTTCAGCTTTCTCATGAGGCAATCTACTTTCCTCAGTCTGGGGCTCAGAGTC 99
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Db 1077 GTTCAGCTTTCTCTGCGGGCCCTTTCGCTCAGCTTCTGCGCCAGGGGCT 1018
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QY 100 CCGGGCCAGAT 111
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Db 1017 CCCAGCCAGAT 1006
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RESULT 14
US-09-864-761-5516/C
Sequence 5516, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
```

```
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
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1 PRIOR FILING DATE: 2001-01-30
2 PRIOR APPLICATION NUMBER: US 60/234,687
3 PRIOR FILING DATE: 2000-09-21
4 PRIOR APPLICATION NUMBER: US 09/608,408
5 PRIOR FILING DATE: 2000-06-30
6 PRIOR APPLICATION NUMBER: US 09/774,203
7 PRIOR FILING DATE: 2001-01-29
8 NUMBER OF SEQ ID NOS: 49117
9 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
10 SEQ ID NO 5516
11
12 LENGTH: 472
13
14 TYPE: DNA
15
16 ORGANISM: Homo sapiens
17
18 FEATURE:
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20 OTHER INFORMATION: MAP TO AC004613.1
21 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL - 2.2
22 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL - 1.7
23 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL - 2
24 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL 2 1.8
25 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL - 2
26 OTHER INFORMATION: EXPRESSED IN BLOOD, SIGNAL - 1.7
27 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL - 1.6
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Qy	55	ATGGGGGAATCTACTTGGTCTCCAGTCCGCGGGGCTGCAGAGTCCCGCCCAAGTC	113
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Db	302	ATGGGGCAAGAGCTCAGTTTCCTCTCGTGAATATGACGCACTTATGGCTCGACAAGTTTC	244

Query Match 22.0%; Score 26.6; DB 10; Length 472;
Best Local Similarity 64.4%; P-Ed. No. 7.2;
Matches 38; Conservative 1; Mismatches 20; Indels 0; Gaps 0.

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RESULT 15
US-09-917-800A-61/c
Sequence 61, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917, 800A
CURRENT FILING DATE: 2001-07-31
PRIORITY APPLICATION NUMBER: US 60/222,040
PRIORITY FILING DATE: 2000-07-31
PRIORITY APPLICATION NUMBER: US 60/222,880
PRIORITY FILING DATE: 2000-11-02
PRIORITY APPLICATION NUMBER: US 60/290,029
PRIORITY FILING DATE: 2001-05-11
PRIORITY APPLICATION NUMBER: US 60/290,645
PRIORITY FILING DATE: 2001-05-25
PRIORITY APPLICATION NUMBER: US 60/292,336
PRIORITY FILING DATE: 2001-05-22
PRIORITY APPLICATION NUMBER: US 60/295,798
PRIORITY FILING DATE: 2001-06-06
PRIORITY APPLICATION NUMBER: US 60/297,457
PRIORITY FILING DATE: 2001-06-13
PRIORITY APPLICATION NUMBER: US 60/298,884
PRIORITY FILING DATE: 2001-06-19
PRIORITY APPLICATION NUMBER: US 60/303,459
PRIORITY FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 61
LENGTH: 494
TYPE: DNA
ORGANISM: Rattus norvegicus

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; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 AA818264
US-09-917-800A-61

Query Match      22.0% ; Score 26.6 ; DB 10 ; Length 194 ;
Best Local Similarity 53.3% ; Pred. No. 7.3 ;
Matches 56 ; Conservative 0 ; Mismatches 49 ; Indels 0 ; Gaps 0 ;

Oy      10  CTTGTCCTCCATAGAGAGCCCGAGTGGATTCAGCTTTTCTCATGGGCAATCTYA 69
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      193  CATGGTCTTCTCCATATCTTTTGGGACACAGTGGGACACTCTCTTTGGGAGACCGA 134
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Oy      70  CTTTTCGCTCAGTCTCGGGGCTCAGACGCTCCCTCGCCGAGTCC 114
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      133  CTATTCCTGACAGTCCCTGTGGCCAAATCTCCACCGAGAGAAC 89
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Search completed: November 21, 2002, 03:44:41
Job time : 134 secs

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